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OM protein - protein search, using sw model

Run on: November 12, 2002, 16:48:46 : Search time 70.2833 Seconds
(without alignments)
348.847 Million cell updates/sec

Title: US-09-848-271-2

Sequence: 1 MLOMAGCCSNDYFDLLHA.....CKSIPALATSEIKSISAR 184

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 908470 seqs, 133250620 residues

Total number of hits satisfying chosen parameters: 908470

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 08

Maximum Match 1008

Listing first 45 summaries

Database :

A_Geneseq.101002:*

1: /SID52/gcgdata/geneseq/geneseq-emb1/AA1980.DAT:*

2: /SID52/gcgdata/geneseq/geneseq-emb1/AA1981.DAT:*

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18: /SID52/gcgdata/geneseq/geneseq-emb1/AA1997.DAT:*

19: /SID52/gcgdata/geneseq/geneseq-emb1/AA1998.DAT:*

20: /SID52/gcgdata/geneseq/geneseq-emb1/AA1999.DAT:*

21: /SID52/gcgdata/geneseq/geneseq-emb1/AA2000.DAT:*

22: /SID52/gcgdata/geneseq/geneseq-emb1/AA2001.DAT:*

23: /SID52/gcgdata/geneseq/geneseq-emb1/AA2002.DAT:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	964	100.0	184	21	AA08843	Amino acid sequenc
2	964	100.0	184	21	AAV94001	A human BCMA prote
3	964	100.0	184	22	AAE09241	Human BCMA protein
4	964	100.0	184	22	AAE00506	Human B cell matur
5	964	100.0	184	22	AAE00506	Human B cell matur
6	964	100.0	184	22	AAV71979	Human BAFR recepto
7	964	100.0	184	22	ABB81487	Human BCMA recepto
8	950	98.5	181	23	AAE15484	Human B-cell matur
9	719.5	74.6	157	22	AAE07000	Human BAFR recepto
10	572	59.3	185	21	AA08844	Amino acid sequenc

11	572	59.3	185	22	AAV71980	Murine B cell matu
12	572	59.3	185	23	AAE15490	Mouse B cell matur
13	323	33.5	58	23	AAE15501	Human B cell matur
14	311.5	32.3	117	23	AAE15491	Human-murine B cel
15	286.5	29.7	302	22	AAE00507	Human BCMA-immunog
16	286.5	29.7	302	22	AAE00507	Mouse IgG signal/h
17	285	29.7	283	23	AAE15488	Human BCMA-immunog
18	284	29.5	51	23	AAE15485	Human B-cell matur
19	201	20.9	34	23	AAE15486	Human B-cell matur
20	187	19.4	281	23	AAE15489	Human BCMA-human 1
21	116.5	12.1	175	23	ABB81489	Mouse ztnfr12 prot
22	116.5	12.1	175	23	AAE22244	Murine BAFR recept
23	106.5	11.0	185	23	AAE22266	Human BAFR recepto
24	105.5	10.9	185	23	AAE22267	Human BAFR recepto
25	104	10.8	21	23	AAE15487	Human B-cell matur
26	103.5	10.7	185	23	AAE22269	Human BAFR recepto
27	100.5	10.4	185	23	AAE22271	Human BAFR recepto
28	99.5	10.3	185	23	AAE22268	Human BAFR recepto
29	97.5	10.1	185	23	AAE22270	Human BAFR recepto
30	94.5	9.8	185	23	AAE22242	Human mature JST57
31	93	9.6	184	23	ABB81483	Human ztnfr12 prot
32	93	9.6	266	23	AAE22243	Human JST576 (BAF
33	90.5	9.4	24	23	AAE15492	Human-murine BCMA
34	83.5	8.7	404	23	AAO14136	Protein of a compl
35	82	8.5	1009	19	AAW61196	Mouse protein tyro
36	82	8.5	1009	19	AAW64568	Mouse protein tyr
37	82	8.5	1009	19	AAW48374	Mouse related adhe
38	81	8.4	576	20	AAW23925	Amino acid sequenc
39	79.5	8.2	1009	17	AAU09900	Human AGP-3 relate
40	79.5	8.2	1009	17	AAU09900	Protein tyrosine ki
41	79.5	8.2	1009	19	AAW57891	Human PKC-2 protei
42	79.5	8.2	1009	19	AAW57891	Human related adhe
43	79.5	8.2	857	13	AAK28814	S receptor kinase
44	78.5	8.1	265	22	AAE09244	Human TAC1 splice
45	78.5	8.1	293	19	AAW57883	Human lymphocyte s

ALIGNMENTS

RESULT 1	
AA08843	
ID	AA08843 standard; peptide; 184 AA.
XX	
AC	AA08843:
XX	
DT	02-JAN-2001 (first entry)
XX	
DE	Amino acid sequence of human.
XX	
KW	BCMA: necrosis factor-kB activator; NF-kB; gene expression; cancer;
KW	anti-cell death gene; apoptosis; viral infection; inflammatory response;
RW	rheumatoid arthritis; inflammatory bowel disease; septic shock.
XX	
OS	Homo sapiens.
XX	
FT	Key
FT	Domain
XX	
PN	WO200050633-A1.
PD	31-AUG-2000.
XX	
PE	24-FEB-2000; 2000MO-US04925.
XX	
PR	24-FEB-1999; 99US-0121485.
PA	(GENO) GEN HOSPITAL CORP.
XX	
PI	Seed B, Ting A;
XX	
DR	WPI: 2000-558405/51.

XX Identifying a modulator of gene expression for drug designing, by
PT contacting a compound library with a cell expressing an anti-cell death
PT gene and reporter gene, and determining alteration in reporter gene
PS expression
XX
PS Claim 32; Fig 7A; 53pp; English.
XX
CC The present sequence represents a BCMA (not defined) polypeptide. BCMA
CC is a necrosis factor (NF)- κ B activator. The method of the invention is
CC used to identify compounds which modulate BCMA activity (and thus NF- κ B
CC activity). The specification describes a method of identifying a
CC polypeptide which increases gene expression from a promoter. The method
CC involves contacting a library of with a cell which expresses a
CC recombinant anti-cell death gene and a reporter gene operably linked to
CC the promoter, and then determining whether the expression of the
CC reporter gene is altered as a result of contact with library. The method
CC is useful for identifying polypeptides which increase or decrease gene
CC expression from a promoter. The BCMA polypeptide or nucleic acid are
CC useful for preparing a pharmaceutical composition for treating cancer,
CC apoptosis, viral infections, inflammatory response, such as rheumatoid
CC arthritis, inflammatory bowel disease or septic shock. BCMA is useful for
CC identifying compounds that modulate NF- κ B expression and thus for drug
CC designing.
XX
SQ Sequence 184 AA;
Query Match 100.0%; Score 964; DB 21; Length 184;
Best Local Similarity 100.0%; Pred. No. 1.3e-95;
Matches 184; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MLOMAGCQSQNEYFDSLHACIPQALRCSNTPPLTCQRYCNASTVNSVKGNTNATIMTCL 60
DB 1 MLOMAGCQSQNEYFDSLHACIPQALRCSNTPPLTCQRYCNASTVNSVKGNTNATIMTCL 60
QY 61 GLSLIISLAVFVLMFLRKISSEPLKDERFNKSGLLGMANIDLEKSRGDEIILPRL 120
DB 61 GLSLIISLAVFVLMFLRKISSEPLKDERFNKSGLLGMANIDLEKSRGDEIILPRL 120
QY 121 YVEECCTCEDCIKSKPVVSDHCFPLPAMEGATILVTTKTNDYCKSLPALISATEIEKS 180
DB 121 YVEECCTCEDCIKSKPVVSDHCFPLPAMEGATILVTTKTNDYCKSLPALISATEIEKS 180
QY 181 ISAR 184
DB 181 ISAR 184
RESULT 2
AA094001
ID AA094001 standard; Protein; 184 AA.
XX
AC AA094001;
XX
DT 20-OCT-2000 (first entry)
XX
DE A human BCMA protein, a B cell protein related to TACI.
XX
XX Human: BR43x2; TACI receptor; extracellular domain; BCMA; B cell protein;
KW transmembrane activator and CAML-interactor; tumour necrosis factor; TNF;
KW zlotif activity; antibody production; autoimmune disease; amyloidosis;
KW systemic lupus erythematosus; myasthenia gravis; multiple sclerosis;
KW rheumatoid arthritis; asthma; bronchitis; emphysema; pyelonephritis;
KW end stage renal failure; glomerulonephritis; vasculitis; nephritis;
KW renal neoplasia; multiple myeloma; lymphoma; light chain neuropathy;
KW immune response; immunosuppression; graft rejection; joint pain;
KW graft versus host disease; inflammation; swelling; anaemia; septic shock;
KW insulin dependent diabetes mellitus; Crohn's disease; hypertension;
KW renal artery stenosis; occlusion; cholesterol; renal emboli.
XX
XX Homo sapiens.
OS
XX
PN WO200040716-A2.

XX
PD 13-JUL-2000.
XX
XX 07-JAN-2000; 2000WD-US00396.
XX
XX 07-JAN-1999; 99US-0226533.
XX
XX
XX (ZYMO) ZYMOGENETICS INC.
XX
XX Gross JA, Xu W, Madden K, Yee DP;
PI
XX
XX WPI: 2000-452538/39.
XX
XX N-PSDB; AAS58559.
XX
XX Inhibiting ztnf4 activity in a mammal, to treat autoimmune diseases,
PT renal disease, graft versus host disease, and inflammation, comprises
PT administering a BR43x2, TACI or BCMA extracellular domain polypeptide -
PS Disclosure: Page 152; 175pp; English.
XX
XX The present sequence represents a human BCMA protein, a B cell protein
XX related to transmembrane activator and CAML-interactor (TACI) receptor.
XX TACI is a tumour necrosis factor (TNF) receptor. The extracellular
XX domain of BR43x2 (an isoform of TACI), TACI or BCMA (a related B cell
XX protein) receptor contain a cysteine rich domain, and are used for
XX inhibiting ztnf4 activity. ztnf4 is a TNF ligand. They may also be used
XX for inhibiting BR43x2, TACI or BCMA receptor-ligand engagement associated
XX with activated or resting B lymphocytes, effector T-cells, or with
XX antibody production. The antibody production is associated with an
XX autoimmune disease selected from systemic lupus erythematosus, myasthenia
XX gravis, multiple sclerosis and rheumatoid arthritis. The ztnf4 activity
XX and BR43x2, TACI or BCMA receptor-ligand engagement is associated with
XX asthma, bronchitis, emphysema, end stage renal failure,
XX glomerulonephritis, vasculitis, nephritis, pyelonephritis, renal
XX amyloidosis, multiple myelomas, lymphomas, light chain neuropathy,
XX antioidosis, moderating immune response, immunosuppression, graft
XX rejection, graft versus host disease, inflammation, insulin dependent
XX diabetes mellitus, Crohn's disease, joint pain, swelling, anaemia, or
XX septic shock. BR43x2, TACI, and BCMA polypeptides, fusions, antibodies,
XX agonists or antagonists can be used to treat hypertension, renal artery
XX stenosis, or occlusion, and cholesterol or renal emboli.
SQ Sequence 184 AA;
Query Match 100.0%; Score 964; DB 21; Length 184;
Best Local Similarity 100.0%; Pred. No. 1.3e-95;
Matches 184; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MLOMAGCQSQNEYFDSLHACIPQALRCSNTPPLTCQRYCNASTVNSVKGNTNATIMTCL 60
DB 1 MLOMAGCQSQNEYFDSLHACIPQALRCSNTPPLTCQRYCNASTVNSVKGNTNATIMTCL 60
QY 61 GLSLIISLAVFVLMFLRKISSEPLKDERFNKSGLLGMANIDLEKSRGDEIILPRL 120
DB 61 GLSLIISLAVFVLMFLRKISSEPLKDERFNKSGLLGMANIDLEKSRGDEIILPRL 120
QY 121 YVEECCTCEDCIKSKPVVSDHCFPLPAMEGATILVTTKTNDYCKSLPALISATEIEKS 180
DB 121 YVEECCTCEDCIKSKPVVSDHCFPLPAMEGATILVTTKTNDYCKSLPALISATEIEKS 180
QY 181 ISAR 184
DB 181 ISAR 184
RESULT 3
AAE09241
ID AAE09241 standard; Protein; 184 AA.
XX
XX AAE09241;
AC
XX
DT 19-NOV-2001 (first entry)
XX

DE Human BCMA protein.
XX
XX Human; TNF; tumour necrosis factor; TALL-1; APRIL; TNF receptor;
KW TNFR; TACI; BCMA; therapy; cancer; leukaemia; myeloma; lymphoma;
KW autoimmune disease; rheumatoid arthritis; multiple sclerosis;
KW psoriasis.
XX
XX Homo sapiens.
OS
XX WO200160397-A1.
XX
XX 23-AUG-2001.
XX
XX 28-NOV-2000; 2000WO-US32378.
XX
XX 16-FEB-2000; 2000US-0182938.
XX 22-AUG-2000; 2000US-0226986.
XX
XX (GETH) GENENTECH INC.
XX
XX Ashkenazi AJ, Dodge KH, Grewal I, Kim KJ, Marsters SA, Pitti RM;
PI Yan M;
XX
XX WPI: 2001-541628/60.
DR N-PSDB: AAD15902.
XX
XX Inhibiting or neutralizing TALL-1 or APRIL polypeptide biological
PT activity, for treating autoimmune disorders and cancer, comprises
PT exposing the cells to TALL-1 or APRIL polypeptide agonists or
PT antagonists -
XX
XX Example 2; Fig 2; 16pp; English.
XX
XX The invention relates to methods of using one or more agonists or
CC antagonists to modulate the activity of the members of TNF (tumour
CC necrosis factor) especially TALL-1, APRIL and TNF receptor (TNFR)
CC e.g. TACI or BCMA. The method is useful for treating pathological
CC conditions or diseases associated with increased TALL-1 and APRIL
CC expression or activity. TALL-1 and APRIL antagonists are used to
CC block the interaction between APRIL and TALL-1 with TACI or BCMA.
CC They are useful for treating a mammal suffering from cancer such
CC as leukaemia, lymphoma, myeloma, cancers of lung and colon and
CC autoimmune diseases e.g. rheumatoid arthritis, multiple sclerosis,
CC psoriasis and lupus erythematosus. The present sequence is human
CC BCMA protein.
XX
XX
SQ Sequence 184 AA;
Query Match 100.0%; Score 964; DB 22; Length 184;
Best Local Similarity 100.0%; Pred. No. 1,3e-95;
Matches 184; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

AC AAE00506;
XX
XX 31-JUL-2001 (first entry)
DT
XX
XX Human B cell maturation protein (BCMA).
DE
XX
XX Human; A proliferation inducing ligand Receptor; APRIL-R; cytostatic;
KW gene therapy; cancer; nephrotropic; renal disorder; autoimmune disease;
KW carcinoma; lung; colon; breast; prostate; Grave's disease; hypertension;
KW systemic lupus erythematosus; SLE; inflammation; cardiovascular disease;
KW B-cell lympho-proliferative disorder; BCM; immunosuppressive disease;
KW organ transplantation; HIV; human immunodeficiency virus; TNF;
KW tumour necrosis factor; BCMA; B cell maturation protein.
XX
XX Homo sapiens.
OS
XX WO200124811-A1.
XX
XX 12-APR-2001.
XX
XX 05-OCT-2000; 2000WO-US27579.
XX
XX 06-OCT-1999; 99US-0157933.
XX 11-FEB-2000; 2000US-0181807.
XX 30-JUN-2000; 2000US-0215868.
XX
XX (BIOJ) BIOGEN INC.
XX (APOT-) APOTEC R & D SA.
XX
XX Schneider P, Thompson J, Cachero T, Ambrose C, Rennert P;
PI
XX WPI: 2001-266342/27.
DR N-PSDB: AAD03844.
XX
XX Treating a mammal for a condition associated with undesired cell
PT proliferation such as cancer or carcinoma, comprises administering a
PT composition comprising A Proliferation Inducing Ligand Receptor
PT (APRIL-R) antagonist -
XX
XX
PS Claim 3; Fig 3A; 85pp; English.
XX
XX The invention relates to a method of treating a mammal for a condition
CC associated with undesired cell proliferation such as cancer or
CC carcinoma. The method involves administering a composition comprising
CC A Proliferation Inducing Ligand Receptor (APRIL-R) also referred as
CC B cell maturation protein (BCM or BCMA) antagonist that antagonises the
CC interaction between APRIL and its cognate receptor(s). This method is
CC useful for treating undesired cell proliferation such as cancer or
CC carcinoma e.g. human lung carcinoma, colon carcinoma, breast carcinoma,
CC prostate carcinoma, and other carcinomas whose proliferation is modulated
CC by APRIL. It is also useful for treating autoimmune diseases (Grave's
CC disease, systemic lupus erythematosus-SLE); hypertension, cardiovascular
CC diseases, renal disorders, B-cell lympho-proliferative disorders,
CC immunosuppressive diseases, organ transplantation, inflammation and
CC human immunodeficiency virus (HIV), and for treating, suppressing or
CC altering an immune response involving a signalling pathway between
CC APRIL-R and its ligand. APRIL-R DNA is also useful in gene therapy.
CC The present sequence is human APRIL-R also referred as BCMA or
CC BCM protein.
XX
XX
SQ Sequence 184 AA;
Query Match 100.0%; Score 964; DB 22; Length 184;
Best Local Similarity 100.0%; Pred. No. 1,3e-95;
Matches 184; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY	121	YTVVEECGCECCIKSRKPKVDSDHCPPLAMEEGATILVTTKTDYCKSLPALSATETIENS	180
Db	121	YTVVEECGCECCIKSRKPKVDSDHCPPLAMEEGATILVTTKTDYCKSLPALSATETIENS	180
OY	181	ISAR 184	
Db	181	ISAR 184	
RESULT 5			
AAB60698			
ID	AAB60698	standard: Protein: 184 AA.	
XX			
AC	AAB60698:		
XX			
DT	22-MAY-2001	(first entry)	
XX			
DE	Human BAFf receptor (BAFf-R).		
XX			
KW	Human BAFf-R: BAFf receptor; TNF family; immunoregulatory agent;		
KW	immune-related disorder; B-cell growth inhibitor; BCMA:		
KW	B-cell maturation inhibitor; immunoglobulin production inhibitor;		
KW	autoimmune disorder; B-cell lymphoproliferative disorder; hyperextension;		
KW	organ transplantation; immunosuppressive disorder; HIV infection;		
KW	renal transplantation; antiinflammatory; systemic lupus erythematosus;		
KW	autoimmune haemolytic anaemia; grave's disease; multiple myeloma;		
KW	B-cell carcinoma; leukaemia; rapidly progressive glomerulonephritis;		
KW	lymphoma; gene therapy; cancer; tumour.		
XX			
OS	Homo sapiens.		
XX			
PN	WO200112812-A2.		
XX			
PD	22-FEB-2001.		
XX			
PE	16-AUG-2000; 2000WO-US22507.		
PR	17-AUG-1999; 99US-0149378.		
PR	11-FEB-2000; 2000US-0181684.		
PR	18-FEB-2000; 2000US-0183536.		
XX			
PA	(AIOT) BIOGEN INC.		
PA	(APOT-) APOTEC R & D SA.		
PI	MacKay F, Browning J, Ambrose C, Tschopp J, Schneider P;		
PI	Thompson J;		
XX			
DR	WPI: 2001-202866/20.		
DR	N-PSDB: AAF59988.		
XX			
PT	Inhibiting dendritic cell-induced B-cell growth, maturation and B-cell		
PT	lympho-proliferative disorder by administering BAFf-receptor		
PT	polypeptide, chimeric molecule comprising receptor or anti-BAFf-R		
PT	antibody homolog -		
XX			
PS	Claim 20; Fig 1; 59pp: English.		
XX			
XX	The invention relates to the use of a BAFf receptor (BAFf-R, also known		
XX	as BCMA) protein, or a BAFf-R fusion protein as an agent for the		
CC	treatment of a variety of immune-related disorders. BAFf-R is a member of the		
CC	TNF (tumour necrosis factor) family, acting as an immunoregulatory		
CC	agent, and also plays a role in the development of hypertension and		
CC	related disorders. BAFf-R, fusion proteins containing it, and BAFf-R-		
CC	specific antibodies can be used for inhibiting B-cell growth, dendritic		
CC	cell-induced B-cell growth and maturation, and immunoglobulin production,		
CC	and in the treatment of autoimmune disorders, B-cell lymphoproliferative,		
CC	disorders, hypertension and renal disorders. The BAFf-R proteins may also		
CC	be used in the treatment of immunosuppressive disorders and HIV		
CC	infection, and in patients undergoing organ transplantation. The BAFf-R		
CC	proteins or BAFf-R specific antibodies may be used for treating,		
CC	suppressing or altering an immune response involving a signalling pathway		
CC	between BAFf-R and BAFf, thereby inhibiting inflammation. Since BAFf-R		

CC	inhibits B-cell growth and maturation. It is useful for treating diseases
CC	such as systemic lupus erythematosus, autoimmune haemolytic anaemia,
CC	grave's disease, multiple myeloma, B-cell carcinomas, leukaemia, rapidly
CC	progressive glomerulonephritis, and lymphomas. Nucleic acids encoding
CC	human BAFF-R may be used in gene therapy to treat tumours, lymphomas,
CC	autoimmune disorders and inherited B-cell-associated disorders. The
CC	present sequence represents human BAFF-R.
XX	
SO	Sequence 184 AA:
	Query Match 100.0%; Score 964; DB 22; Length 184;
	Best Local Similarity 100.0%; Pred. No. 1.3e-95;
	Matches 184; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY	1 MLOWAGGCSQNEFFDSLHACIPCOLRCSSNPTLTCORCYNASVTSVYGNATIMTCL 60
DB	1 MLOWAGGCSQNEFFDSLHACIPCOLRCSSNPTLTCORCYNASVTSVYGNATIMTCL 60
OY	61 GLSIIISLAVFVLMFLRKISSEPLKDEFKNTGSGLLGMANIDKESRTGDEITLPRGLE 120
DB	61 GLSIIISLAVFVLMFLRKISSEPLKDEFKNTGSGLLGMANIDKESRTGDEITLPRGLE 120
OY	121 YTYEECTCEGCIKSKRPVDSDDHCFPLPAHEEGCATILVTTKTNDYCKSLPALASATRIEKS 180
DB	121 YTYEECTCEGCIKSKRPVDSDDHCFPLPAHEEGCATILVTTKTNDYCKSLPALASATRIEKS 180
OY	181 ISAR 184
DB	181 ISAR 184
RESULT 6	
ID	AAV71979
AC	AAV71979 standard; Protein; 184 AA.
XX	
XX	AAV71979;
XX	
XX	28-MAR-2001 (first entry)
DE	
XX	
XX	Human B cell maturation factor (BCMA) protein.
KW	Human: Tumour Necrosis Factor; TNF; immunosuppressant; TALL-1;
KW	Tumour necrosis factor and Apol-related leucocyte expressed ligand 1;
KW	therapy; autoimmune disorder; rheumatoid arthritis; multiple sclerosis;
KW	systemic lupus erythematosus; SLE; insulin dependent diabetes mellitus;
KW	thrombocytopenia purpura; acute rheumatic fever; Goodpasture's syndrome;
KW	hemolytic anaemia; Grave's disease; myasthenia gravis; chromosome 16;
KW	post-streptococcal glomerulonephritis; polyarteritis nodosa; BCMA;
KW	B cell maturation factor; pemphigus vulgaris; B-lymphocyte proliferation.
XX	
OS	Homo sapiens.
XX	
XX	
FH	Key Location/Qualifiers
FT	1..62
FT	Domain
XX	
XX	WO200068378-A1.
XX	
XX	16-NOV-2000.
XX	
XX	05-MAY-2000: 2000MO-US12266.
XX	
XX	06-MAY-1999: 99US-0132892.
XX	
XX	01-MAY-2000: 2000US-0201012.
XX	
XX	(NAJE-) NAT JEWISH MEDICAL & RES CENT.
XX	
XX	Shu HS:
XX	
XX	
XX	WPI: 2001-016094/02.
XX	
XX	N-PSDB: AAD02125.
XX	
XX	Isolated TALL-1 protein is used to identify compounds that regulate B

PT	lymphocyte proliferation, used to treat B lymphocyte associated
PT	autoimmune disorders -
XX	
XX	
PS	Claim 37: page 104-105; 112pp; English.
CC	The present invention relates to Tumour necrosis factor (TNF) and
CC	Apol-related Leucocyte expressed Ligand 1 (TALL-1) nucleic acid
CC	molecules, proteins (including homologues), and their antibodies. The
CC	invention in particular relates to methods for regulating the
CC	interaction between TALL-1 and TALL-1 receptors (BCMA referred as B cell
CC	maturation factor) to regulate monocyte, macrophage and B lymphocyte
CC	mediated immune responses. TALL-1 protein is useful for identifying
CC	compounds that regulate B lymphocyte proliferation. It is also useful for
CC	treating B lymphocyte associated autoimmune disorders like rheumatoid
CC	arthritis, systemic lupus erythematosus (SLE), insulin dependent diabetes
CC	mellitus, multiple sclerosis, myasthenia gravis, Grave's disease,
CC	autoimmune haemolytic anaemia, autoimmune thrombocytopenia purpura,
CC	Goodpasture's syndrome, pemphigus vulgaris, acute rheumatic fever,
CC	post-streptococcal glomerulonephritis, or polyarthritis nodosa.
CC	The TALL-1 protein and its corresponding nucleic acid sequence are also
CC	useful in diagnostic assays.
CC	The present sequence is a human B cell maturation factor (BCMA)
CC	protein. It is the receptor for TALL-1 protein. BCMA gene is
CC	located on chromosome 16. In human tissues, BCMA is expressed by
CC	spleen and lymph nodes but not by brain, muscle, heart, lung, kidney,
CC	pancreas, testis and placenta. BCMA mRNA is absent in the pro-B
CC	lymphocyte stage but its expression increases with B lymphocyte
CC	maturation.
CC	
XX	
SO	Sequence 184 AA;
	Query Match 100.0%; Score 964; DB 22; Length 184;
	Best Local Similarity 100.0%; Pred. No.1.3e-95;
	Matches 184; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY	1 MLOWAGGSGSNEFDSLHACIPGCRGSSNPPILTCGRGMAVTSVGTNAILMTCL 60
DB	1 MLOWAGGSGSNEFDSLHACIPGCRGSSNPPILTCGRGMAVTSVGTNAILMTCL 60
OY	61 GLSLITISLAVFLVLMFLLRKISSEPLKDEEKNFGSGLGMANIDLEKSNRGDEITLPGLE 120
DB	61 GLSLITISLAVFLVLMFLLRKISSEPLKDEEKNFGSGLGMANIDLEKSNRGDEITLPGLE 120
OY	121 YTVEECCGCEGCIKSKPVDSGDHCFPLPAEEGATILVYTKINDCKSLPALASTIEKRS 180
DB	121 YTVEECCGCEGCIKSKRVDSGDHCFPLPAEEGATILVYTKINDCKSLPALASTIEKRS 180
OY	181 ISAR 184
DB	181 ISAR 184
RESULT 7	
ID	ABB81487 standard: Protein; 184 AA.
XX	ABB81487;
AC	
XX	
DE	02-SEP-2002 (first entry)
XX	
XX	Human BCMA receptor related protein SEQ ID NO:7.
XX	
XX	Human: ZNF112; tumour necrosis factor receptor; cytostatic;
KM	Immunosuppressive; dermatological; antiinflammatory; antidiabetic;
KM	neuroprotection; antirheumatic; antiarthritis; antiasthmatic;
KM	nephrotic; hypotensive; gene therapy; B lymphocyte; tumour;
KM	autoimmune disorder; systemic lupus erythematosus; myasthenia gravis;
KM	multiple sclerosis; insulin dependent diabetes mellitus; asthma;
KM	rheumatoid arthritis; bronchitis; emphysema; renal disease; lymphoma;
KM	glomerulonephritis; vasculitis; chronic lymphoid leukaemia; nephritis;
KM	pyelonephritis; renal neoplasm; multiple myeloma; amyloidosis;
KM	light chain neuropathy; hypertension; large vessel disease;
KM	graft-versus host disease; graft rejection; Crohn's disease.

AAE15484
ID AAE15484 standard; Protein; 181 AA.
XX
AC AAE15484;
XX
DT 12-MAR-2002 (first entry)
XX
DE Human B-cell maturation (BCMA) protein.
XX
KW Human; transmembrane activator and intracellular CAML interactor; TACI;
KW cytosolic; B cell maturation protein; BCMA; tumor necrosis factor; TNF;
KW lymphoproliferative disorder; tumour; lung; gastrointestinal; pancreatic;
KW prostate; inflammation; immune disorder; diarrhoea; psoriasis; colitis;
KW drug allergy; dermatitis; pneumonia; asthma; inflammatory bowel disease;
KW Crohn's disease; scleroderma; autoimmune disease; multiple sclerosis;
KW human immunodeficiency virus; HIV; systemic lupus erythematosus; cancer;
KW rheumatoid arthritis; atherosclerosis.
XX
OS Homo sapiens.
XX
FI Key
FI Region
FI 5..38
FI /note- "Cysteine-rich consensus region; This is region
FI is specifically claimed as SEQ ID NO: 7 in claim 1 of
FI the specification"
FI 52..72
FI Domain
FI /label- Transmembrane_domain
XX
XX MO200187979-A2.
XX
XX 22-NOV-2001.
XX
XX 14-MAY-2001; 2001MO-US15567.
XX
XX 12-MAY-2000; 2000US-204039P.
XX 27-JUN-2000; 2000US-214591P.
XX 14-MAY-2001; 2001US-0214591.
XX
XX (AMGE-) AMGEN INC.
XX
XX Theell LE, Yu G;
XX
XX WPI; 2002-066686/09.
XX
XX Inhibiting activity of B cell maturation protein and/or transmembrane
XX activator and intracellular cyclophilin ligand interactor, by
XX administering a binding partner for APRIL, a tumor necrosis factor
XX family ligand
XX
XX Disclosure; Fig 10A; 94pp; English.
XX
XX The invention relates to a method for inhibiting TACI (transmembrane
XX activator and intracellular CAML interactor) and/or B cell maturation
XX protein (BCMA) activity in a mammal. The method comprises administering
XX a specific binding partner for APRIL (G70, a tumor necrosis factor-TNF
XX family ligand), having the consensus region of TACI, BCMA, or the TACI/
XX BCMA extracellular consensus sequence, but not the extracellular region
XX of TACI or BCMA. The method is useful for inhibiting activity of TACI
XX and/or BCMA in a mammal which is useful for treating B-cell or T-cell
XX lymphoproliferative disorders, one or more solid tumours such as lung,
XX gastrointestinal, pancreatic or prostate tumour. APRIL, BCMA and TACI
XX antagonists are useful for treating inflammation and immune function
XX diseases such as diarrhoea, psoriasis, allergies, pneumonia, atopic
XX dermatitis, respiratory allergic disease (asthma, hypersensitivity lung
XX disease), drug and insect sting allergy, inflammatory bowel disease
XX (Crohn's disease, colitis), scleroderma, autoimmune disease (multiple
XX sclerosis, Rheumatoid arthritis, systemic lupus erythematosus), fungal,
XX bacterial, protozoal and viral infections (HIV), atherosclerosis, cancer
XX with leucocyte infiltration of the skin or organs. The present sequence
XX is human BCMA protein.
XX
XX Sequence 181 AA:

Query Match 98.5%; Score 950; DB 23; Length 181;
Best Local Similarity 100.0%; Pred No. 4e-94;
Matches 181; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 4 MAGGCSONEYRDSLLHACIPCOLRCSNTPPLTCORYCNASVTNSVKTNAILMTGCLGS 63
DB 1 MAGGCSONEYRDSLLHACIPCOLRCSNTPPLTCORYCNASVTNSVKTNAILMTGCLGS 60
OY 64 LIISLAVFLMFLRKISSRPLKDEFRKNTGSGILGMANIDLEKSRTPGEIILPGLETV 123
DB 61 LIISLAVFLMFLRKISSRPLKDEFRKNTGSGILGMANIDLEKSRTPGEIILPGLETV 120
OY 124 EECCEDCIKSRKPVDSDDCPPLPAMEGATILVTTKINDYCKSLPALSAETEKSISA 183
DB 121 EECCEDCIKSRKPVDSDDCPPLPAMEGATILVTTKINDYCKSLPALSAETEKSISA 180
OY 184 R 184
DB 181 R 181
RESULT 9
AAB60700
ID AAB60700 standard; Protein; 157 AA.
XX
AC AAB60700;
XX
XX 22-MAY-2001 (first entry)
XX
XX Human BAFF receptor (BAFF-R) sequence encoded by A plasmid pJST535.
XX
XX Human BAFF-R; BAFF receptor; TNF family; immunoregulatory agent;
XX immune-related disorder; B-cell growth inhibitor; BCMA;
XX B-cell maturation inhibitor; immunoglobulin production inhibitor;
XX autoimmune disorder; B-cell lymphoproliferative disorder; hypertension;
XX renal disorder; immunosuppressive disorder; HIV infection;
XX organ transplantation; antiinflammatory; systemic lupus erythematosus;
XX autoimmune hemolytic anaemia; Grave's disease; multiple myeloma;
XX B-cell carcinoma; leukaemia; rapidly progressive glomerulonephritis;
XX lymphoma; gene therapy; cancer; tumour; plasmid pJST535.
XX
XX Homo sapiens.
XX
XX MO200112812-A2.
XX
XX 22-FEB-2001.
XX
XX 16-AUG-2000; 2000MO-US22507.
XX
XX 17-AUG-1999; 99US-0149378.
XX 11-FEB-2000; 2000US-0181684.
XX 18-FEB-2000; 2000US-0183536.
XX
XX (BIOJ) BIOGEN INC.
XX (APOT-) APOTEC R & D SA.
XX
XX Mackay F, Browning J, Ambrose C, Tschopp J, Schneider P;
XX Thompson J;
XX WPI; 2001-202866/20.
XX N-PSDB; AAF60000.
XX
XX Inhibiting dendritic cell-induced B-cell growth, maturation and B-cell
XX lympho-proliferative disorder by administering BAFF-receptor
XX polypeptide, chimeric molecule comprising receptor or anti-BAFF-R
XX antibody homolog
XX
XX Example 1; Fig 3; 59pp; English.
XX
XX The invention relates to the use of a BAFF receptor (BAFF-R, also known
XX as BCMA) protein, or a BAFF-R fusion protein as an agent for the
XX treatment of a variety of immune-related disorders. BAFF-R is a member of
XX the TNF (tumour necrosis factor) family, acting as an immunoregulatory

CC agent, and also plays a role in the development of hypertension and
 CC related disorders. BAFF-R, fusion proteins containing It, and BAFF-R-
 CC specific antibodies can be used for inhibiting B-cell growth, dendritic
 CC cell-induced B-cell growth and maturation, and immunoglobulin production,
 CC and in the treatment of autoimmune disorders, B-cell lymphoproliferative
 CC disorders, hypertension and renal disorders. The BAFF-R proteins may also
 CC be used in the treatment of immunosuppressive disorders and HIV
 CC infection, and in patients undergoing organ transplantation. The BAFF-R
 CC proteins or BAFF-R specific antibodies may be used for treating,
 CC suppressing or altering an immune response involving a signalling pathway
 CC between BAFF-R and BAFF, thereby inhibiting inflammation. Since BAFF-R
 CC inhibits B-cell growth and maturation it is useful for treating diseases
 CC such as systemic lupus erythematosus, autoimmune haemolytic anaemia,
 CC Grave's disease, multiple myeloma, B-cell carcinomas, leukaemia, rapidly
 CC progressive glomerulonephritis, and lymphomas. Nucleic acids encoding
 CC human BAFF-R may be used in gene therapy to treat tumours, lymphomas,
 CC autoimmune disorders and inherited B-cell-associated disorders. The
 CC present sequence represents a human BAFF-R protein sequence as encoded
 CC by plasmid pU5735. However, this BAFF-R protein sequence is 27 amino
 CC acids shorter than that given in AAB60698.

CC Sequence 157 AA;

Query Match Best Local Similarity 74.6%; Score 719.5; DB 22; Length 157;
 Matches 157; Conservative 0; Mismatches 0; Indels 27; Gaps 9;

0Y 1 MLOMAGCCSQNEVEFDLSLHACIPCOLRCSSNTPPLTCQRYCNASYNSVKGYNALMTCL 60
 DB 1 MLOMAG---ONEYFDLSLHACIPCOLR---NPPPLTCQRYCNASYTN---GNATLMTCL 51

0Y 61 GLSLITSLAVFVLMFLRKISSEPTLDEFNKSGLLGMANIDLEKSTGEGITLPRGL 120
 DB 52 GLSLITIS---FVLMFLRKISSEPTLND---NIGSLGMANIDLEK---DEITLPRGLE 102

0Y 121 YTYVEECTCEDCIKSKRPVDSHDCFPPLAMEGATILVTTKTDYCKSLPAALSAATEIKS 180
 DB 103 YTYVEECT---CIKSKRPVDSHDCFPPLP---EGATILVTTKTDYCKS---ALSATEIKS 153

0Y 181 ISAR 184
 DB 154 ISAR 157

RESULT 10
 AAB08844
 ID AAB08844 standard; peptide; 185 AA.

AC AAB08844;
 DT 02-JAN-2001 (first entry)

DE Amino acid sequence of murine BCMA polypeptide.

XX BCMA; necrosis factor- κ B activator; NF- κ B; gene expression; cancer;
 XX anti-cell death gene; apoptosis; viral infection; inflammatory response;
 XX rheumatoid arthritis; inflammatory bowel disease; septic shock.

OS Mus musculus.

XX Key Location/Qualifiers
 XX Domain 47..72 /note="putative transmembrane domain"

XX MO200050633-A1.

XX 31-AUG-2000.

XX 24-FEB-2000; 2000MO-US04925.

XX 24-FEB-1999; 99US-0121485.

XX (GEHO) GEN HOSPITAL CORP.

XX Seed B, Ting A;
 PI WPI: 2000-558405/51.

PT Identifying a modulator of gene expression for drug designing, by
 PT contacting a compound library with a cell expressing an anti-cell death
 PT gene and reporter gene, and determining alteration in reporter gene
 PT expression
 PS Claim 32; Fig 7B; 53pp; English.

CC The present sequence represents a BCMA (not defined) polypeptide. BCMA
 CC is a necrosis factor (NF)- κ B activator. The method of the invention is
 CC used to identify compounds which modulate BCMA activity (and thus NF- κ B
 CC activity). The specification describes a method of identifying a
 CC polypeptide which increases gene expression from a promoter. The method
 CC involves contacting a library of with a cell which expresses a
 CC recombinant anti-cell death gene and a reporter gene operably linked to
 CC the promoter, and then determining whether the expression of the
 CC reporter gene is altered as a result of contact with library. The method
 CC is useful for identifying polypeptides which increase or decrease gene
 CC expression from a promoter. The BCMA polypeptide or nucleic acid are
 CC useful for preparing a pharmaceutical composition for treating cancer,
 CC apoptosis, viral infections, inflammatory response, such as rheumatoid
 CC arthritis, inflammatory bowel disease or septic shock. BCMA is useful for
 CC identifying compounds that modulate NF- κ B expression and thus for drug
 CC designing.

CC Sequence 185 AA;

Query Match Best Local Similarity 59.3%; Score 572; DB 21; Length 185;
 Matches 117; Conservative 21; Mismatches 41; Indels 8; Gaps 4;

0Y 4 MNGCCSQNEVEFDLSLHACIPCOLRCSSNTPPLTCQRYCNASYNSVKGYNALMTCLGSL 63
 DB 1 MNGCCFSEVEFDLSLHACIPCLRCNSN---PPATCQRYCDPSTVSSVKGYYVLMFLGLT 58

0Y 64 LIISLAVFVLMFLRKISSEPTLDEFNKSGLLGMANIDLEKSTGEGITLPRGL 119
 DB 59 LVLSTLALFTTISFLRKIMPEALKDEPOSPOGLKADDELRLRIAGDRITFPLSL 118

0Y 120 YTYVEECTCEDCIKSKRPVDSHDCFPPLAMEGATILVTTKTDYCKSLPAALSAATEI 177
 DB 119 YTYVEECTCEDCVKSKRPVDSHDCFPPLAMEGATILVTTKTDYCKSGKSSVPALGVSVMG 178

0Y 178 EKSIAR 184
 DB 179 EKPTFR 185

RESULT 11
 AAY71980
 ID AAY71980 standard; protein; 185 AA.

AC AAY71980;

DT 28-MAR-2001 (first entry)

DE Murine β cell maturation factor (BCMA) protein.

XX Murine; Tumour Necrosis Factor; TNF; immunosuppressant; TALL-1;
 XX Tumour necrosis factor and Apoc-related leucocyte expressed ligand 1;
 XX therapy; autoimmune disorder; rheumatoid arthritis; multiple sclerosis;
 XX systemic lupus erythematosus; SLE; insulin dependent diabetes mellitus;
 XX thrombocytopenia purpura; acute rheumatic fever; Goodpasture's syndrome;
 XX haemolytic anaemia; Grave's disease; myasthenia gravis; BCMA;
 XX B cell maturation factor; pemphigus vulgaris; B-lymphocyte proliferation;
 XX post-streptococcal glomerulonephritis; polyarteritis nodosa.

XX Mus musculus.

PN W020068378-A1.
 XX 16-NOV-2000.
 XX 05-MAY-2000; 2000MO-US12266.
 XX 06-MAY-1999; 99US-0132892.
 PR 01-MAY-2000; 2000US-0201012.
 XX (NAME-) NAT JEWISH MEDICAL & RES CENT.
 PA Shu HS;
 PI WPI: 2001-016094/02.
 DR N-PSDB; AAD02130.
 PT Isolated TALL-1 protein is used to identify compounds that regulate B
 PT lymphocyte proliferation, used to treat B lymphocyte associated
 PT autoimmune disorders -
 XX Claim 37; Page 107-108; 112pp; English.
 XX The present invention relates to Tumour necrosis factor (TNF) and
 CC Apol-related leucocyte expressed ligand 1 (TALL-1) nucleic acid
 CC molecules, proteins (including homologues), and their antibodies. The
 CC invention in particular relates to methods for regulating the
 CC interaction between TALL-1 and TALL-1 receptors (BCMA referred as B cell
 CC maturation factor) to regulate monocyte, macrophage and B lymphocyte
 CC mediated immune responses. TALL-1 protein is useful for identifying
 CC compounds that regulate B lymphocyte proliferation. It is also useful for
 CC treating B lymphocyte associated autoimmune disorders like rheumatoid
 CC arthritis, systemic lupus erythematosus (SLE), insulin dependent diabetes
 CC mellitus, multiple sclerosis, myasthenia gravis, Grave's disease,
 CC autoimmune haemolytic anaemia, autoimmune thrombocytopenia purpura,
 CC Goodpasture's syndrome, pemphigus vulgaris, acute rheumatic fever,
 CC post-streptococcal glomerulonephritis, or polyarteritis nodosa.
 CC The TALL-1 protein and its corresponding nucleic acid sequence are also
 CC useful in diagnostic assays.
 CC The present sequence is a murine B cell maturation factor (BCMA).
 CC BCMA is the receptor for TALL-1 protein.
 XX Sequence 185 AA:
 SO
 Query Match 59.3%; Score 572; DB 22; Length 185;
 Best Local Similarity 62.6%; Pred. No. 2.1e-53;
 Matches 117; Conservative 21; Mismatches 41; Indels 8; Gaps 4;

QY 4 MAGOCSQNEYFDSLHACIPQOLRCSSNTPLTCQRCNMSVYNSVKTNAIMTCLGLS 63
 DB 1 MAQCCHSEYFDSLHACKPCHLRCSN--PPATCQPCDPSVTSVKGITVLMIFLGLT 58
 QY 64 LITSLAVFLMLFKRISSEPLKDFKN---TSSGILGMANIDLEKSRGTDEIILPRGL 119
 DB 59 LVLSIALFLTISFLRKMPKALDEKDEPQGLDSSAQDLADKADLRLIRAGDRIRFPRSL 118
 QY 120 EYVEBCTCEDCIRKSPYVSDHCFPLPAMEGATILVTTKTDYCK-SLPAAL-SATBI 177
 DB 119 EYVEBCTCEDCIRKSPYVSDHCFPLPAMEGATILVTTKTDYCKSSVPALOSVGMK 178
 QY 178 EKSIAR 184
 DB 179 EKPTHTR 185
 RESULT 12
 ID AAE15490
 AC AAE15490 standard; Protein: 185 AA.
 XX AAE15490;
 DT 12-MAR-2002 (first entry)
 XX Mouse B cell maturation (BCMA) protein.

XX Mouse; transmembrane activator and intracellular CAML interactor; TACI;
 XX cytosolic; B cell maturation protein; BCMA; tumour necrosis factor; TNF;
 KW lymphoproliferative disorder; tumour; lung; gastrointestinal; pancreatic;
 KW prostate; inflammatory; immune disorder; diarrhoea; psoriasis; colitis;
 KW drug allergy; dermatitis; pneumonia; asthma; inflammatory bowel disease;
 KW Crohn's disease; scleroderma; autoimmune disease; multiple sclerosis;
 KW human immunodeficiency virus; HIV; systemic lupus erythematosus; cancer;
 KW rheumatoid arthritis; atherosclerosis.
 XX Mus sp.
 OS
 XX W0200187979-A2.
 XX 22-NOV-2001.
 XX 14-MAY-2001; 2001MO-US15567.
 XX 12-MAY-2000; 2000US-204039P.
 PR 27-JUN-2000; 2000US-214591P.
 PR 14-MAY-2001; 2001US-0214591.
 XX (AMGE-) AMGEN INC.
 PA Thei11 LE, Yu G;
 PI WPI: 2002-066686/09.
 XX Inhibiting activity of B cell maturation protein and/or transmembrane
 PT activator and intracellular cyclophilin ligand interactor, by
 PT administering a binding partner for APRIL, a tumor necrosis factor
 PT family ligand -
 XX Disclosure; Fig 11; 94pp; English.
 XX The invention relates to a method for inhibiting TACI (transmembrane
 CC activator and intracellular CAML interactor) and/or B cell maturation
 CC protein (BCMA) activity in a mammal. The method comprises administering
 CC a specific binding partner for APRIL (G70, a tumour necrosis factor-TNF
 CC family ligand), having the consensus sequence region of TACI, BCMA, or the TACI/
 CC BCMA extracellular consensus sequence, but not the extracellular region
 CC of TACI or BCMA. The method is useful for inhibiting activity of TACI
 CC and/or BCMA in a mammal which is useful for treating B-cell or T-cell
 CC lymphoproliferative disorders, one or more solid tumours such as lung,
 CC gastrointestinal, pancreatic or prostate tumour. APRIL, BCMA and TACI
 CC antagonists are useful for treating inflammation and immune function
 CC diseases such as diarrhoea, psoriasis, allergies, pneumonia, atopic
 CC dermatitis, respiratory allergic disease (asthma, hypersensitivity lung
 CC disease), drug and insect sting allergy, inflammatory bowel disease
 CC (Crohn's disease, colitis), scleroderma, autoimmune disease (multiple
 CC sclerosis, rheumatoid arthritis, systemic lupus erythematosus), fungal,
 CC bacterial, protozoal and viral infections (HIV), atherosclerosis, cancer
 CC with leucocyte infiltration of the skin or organs. The present sequence
 CC is mouse BCMA protein.
 XX Sequence 185 AA:
 SO
 Query Match 59.3%; Score 572; DB 23; Length 185;
 Best Local Similarity 62.6%; Pred. No. 2.1e-53;
 Matches 117; Conservative 21; Mismatches 41; Indels 8; Gaps 4;

QY 4 MAGOCSQNEYFDSLHACIPQOLRCSSNTPLTCQRCNMSVYNSVKTNAIMTCLGLS 63
 DB 1 MAQCCHSEYFDSLHACKPCHLRCSN--PPATCQPCDPSVTSVKGITVLMIFLGLT 58
 QY 64 LITSLAVFLMLFKRISSEPLKDFKN---TSSGILGMANIDLEKSRGTDEIILPRGL 119
 DB 59 LVLSIALFLTISFLRKMPKALDEKDEPQGLDSSAQDLADKADLRLIRAGDRIRFPRSL 118
 QY 120 EYVEBCTCEDCIRKSPYVSDHCFPLPAMEGATILVTTKTDYCK-SLPAAL-SATBI 177
 DB 119 EYVEBCTCEDCIRKSPYVSDHCFPLPAMEGATILVTTKTDYCKSSVPALOSVGMK 178

Oy 178 EKSIAR 184
Db 179 EKPTHR 185

RESULT 13

ID AAE15501 standard; peptide; 58 AA.

AAE15501;

12-MAR-2002 (first entry)

Human B cell maturation protein cysteine rich extracellular region.

Human: transmembrane activator and intracellular CAML interactor; TAC1; cytosolic; B cell maturation protein; BCMA; tumor necrosis factor; TNF; lymphoproliferative disorder; tumour; lung; gastrointestinal; pancreatic; prostate; inflammation; immune disorder; diarrhoea; psoriasis; colitis; drug allergy; dermatitis; pneumonia; asthma; inflammatory bowel disease; Crohn's disease; scleroderma; autoimmune disease; multiple sclerosis; human immunodeficiency virus; HIV; systemic lupus erythematosus; cancer; rheumatoid arthritis; atherosclerosis.

Homo sapiens.

MO200187979-A2.

22-NOV-2001.

14-MAY-2001; 2001MO-US15567.

12-MAY-2000; 2000US-204039P.

27-JUN-2000; 2000US-214591P.

14-MAY-2001; 2001US-0214591.

(AMGE-) AMGEN INC.

The11 LE, Yu G;

WPI: 2002-066686/09.

Inhibiting activity of B cell maturation protein and/or transmembrane activator and intracellular cyclophilin ligand interactor, by administering a binding partner for APRIL, a tumor necrosis factor family ligand
-
Disclosure; Fig 13; 94pp; English.

The invention relates to a method for inhibiting TAC1 (transmembrane activator and intracellular CAML interactor) and/or B cell maturation protein (BCMA) activity in a mammal. The method comprises administering a specific binding partner for APRIL (G70, a tumor necrosis factor-TNF family ligand), having the consensus region of TAC1, BCMA, or the TAC1/BCMA extracellular consensus sequence, but not the extracellular region of TAC1 or BCMA. The method is useful for inhibiting activity of TAC1 and/or BCMA in a mammal which is useful for treating B-cell or T-cell lymphoproliferative disorders, one or more solid tumours such as lung, gastrointestinal, pancreatic or prostate tumour. APRIL, BCMA and TAC1 antagonists are useful for treating inflammation and immune function diseases such as diarrhoea, psoriasis, allergies, pneumonia, atopic dermatitis, respiratory allergic disease (asthma, hypersensitivity lung disease), drug and insect sting allergy, inflammatory bowel disease (Crohn's disease, colitis), scleroderma, autoimmune disease (multiple sclerosis, rheumatoid arthritis, systemic lupus erythematosus), fungal, bacterial, protozoal and viral infections (HIV), atherosclerosis, cancer with leucocyte infiltration of the skin or organs. The present sequence is human BCMA cysteine-rich extracellular region.

Sequence 58 AA;

Query Match 33.5%; Score 323; DB 23; Length 58;
Best Local Similarity 100.0%; Pred. No. 3e-27;

Matches 58; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Oy 8 CSQNEYPDSLHACIPQOLRCSSTPPLTCORYCNASVTNSVKGATNALMTCLSLI 65
Db 1 CSQNEYPDSLHACIPQOLRCSSTPPLTCORYCNASVTNSVKGATNALMTCLSLI 58

RESULT 14

ID AAE15491 standard; Protein; 117 AA.

AAE15491;

12-MAR-2002 (first entry)

Human-murine B cell maturation protein (BCMA) consensus sequence.

Human: transmembrane activator and intracellular CAML interactor; TAC1; cytosolic; B cell maturation protein; BCMA; tumour necrosis factor; TNF; lymphoproliferative disorder; tumour; lung; gastrointestinal; pancreatic; prostate; inflammation; immune disorder; diarrhoea; psoriasis; colitis; drug allergy; dermatitis; pneumonia; asthma; inflammatory bowel disease; Crohn's disease; scleroderma; autoimmune disease; multiple sclerosis; human immunodeficiency virus; HIV; systemic lupus erythematosus; cancer; rheumatoid arthritis; atherosclerosis; mouse.

Chimeric - Homo sapiens.

Chimeric - Mus sp.

MO200187979-A2.

22-NOV-2001.

14-MAY-2001; 2001MO-US15567.

12-MAY-2000; 2000US-204039P.

27-JUN-2000; 2000US-214591P.

14-MAY-2001; 2001US-0214591.

(AMGE-) AMGEN INC.

The11 LE, Yu G;

WPI: 2002-066686/09.

Inhibiting activity of B cell maturation protein and/or transmembrane activator and intracellular cyclophilin ligand interactor, by administering a binding partner for APRIL, a tumor necrosis factor family ligand
-
Disclosure; Fig 11; 94pp; English.

The invention relates to a method for inhibiting TAC1 (transmembrane activator and intracellular CAML interactor) and/or B cell maturation protein (BCMA) activity in a mammal. The method comprises administering a specific binding partner for APRIL (G70, a tumor necrosis factor-TNF family ligand), having the consensus region of TAC1, BCMA, or the TAC1/BCMA extracellular consensus sequence, but not the extracellular region of TAC1 or BCMA. The method is useful for inhibiting activity of TAC1 and/or BCMA in a mammal which is useful for treating B-cell or T-cell lymphoproliferative disorders, one or more solid tumours such as lung, gastrointestinal, pancreatic or prostate tumour. APRIL, BCMA and TAC1 antagonists are useful for treating inflammation and immune function diseases such as diarrhoea, psoriasis, allergies, pneumonia, atopic dermatitis, respiratory allergic disease (asthma, hypersensitivity lung disease), drug and insect sting allergy, inflammatory bowel disease (Crohn's disease, colitis), scleroderma, autoimmune disease (multiple sclerosis, rheumatoid arthritis, systemic lupus erythematosus), fungal, bacterial, protozoal and viral infections (HIV), atherosclerosis, cancer with leucocyte infiltration of the skin or organs. The present sequence is human-murine B cell maturation protein (BCMA) consensus sequence.

Sequence 117 AA;

GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on: November 12, 2002, 16:57:01 ; Search time 25.2704 Seconds
(without alignments)
214.236 Million cell updates/sec

Title: US-09-848-271-2

Perfect score: 964
Sequence: 1 MLOMAGCCSOMEYFDLHA.....CKSLPALSTETKISAR 184

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 262574 segs, 29422922 residues

Total number of hits satisfying chosen parameters: 262574

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 08
Maximum Match 100%
Listing first 45 summaries

Database :
1: /cgn2_6/ptodata/1/aa/5A.COMB.pep.*
2: /cgn2_6/ptodata/1/aa/5B.COMB.pep.*
3: /cgn2_6/ptodata/1/aa/6A.COMB.pep.*
4: /cgn2_6/ptodata/1/aa/6B.COMB.pep.*
5: /cgn2_6/ptodata/1/aa/PCITUS.COMB.pep.*
6: /cgn2_6/ptodata/1/aa/Backfiles1.pep.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	79.5	8.2	1009	2	US-08-357-642A-1
2	79.5	8.2	1009	2	US-08-460-626-1
3	78.5	8.1	293	2	US-08-810-572A-2
4	78.5	8.1	293	4	US-09-290-333-2
5	76	7.9	744	1	US-08-179-481-2
6	75	7.8	854	1	US-07-717-331F-2
7	70.5	7.3	157	4	US-09-233-160-18
8	69.5	7.2	166	2	US-08-810-572A-6
9	69.5	7.2	166	4	US-09-290-333-6
10	69.5	7.2	1180	4	US-08-660-148-2
11	69.5	7.2	1212	4	US-08-660-148-5
12	69.5	7.2	1706	2	US-08-453-568-2
13	69.5	7.2	1706	2	US-08-399-411-2
14	69.5	7.2	1706	3	US-08-516-859A-2
15	69.5	7.2	1706	4	US-09-586-472-2
16	69.5	7.2	1706	4	US-09-528-706-2
17	69.5	7.2	2496	4	US-09-125-028-2
18	69.5	7.2	2958	4	US-08-894-344C-2
19	69	7.2	324	2	US-08-579-940-7
20	69	7.2	445	1	US-08-353-400-33
21	69	7.2	447	6	545030-1
22	69	7.2	464	1	US-08-353-400-36
23	69	7.2	599	1	US-08-442-542-18
24	69	7.2	599	3	US-08-765-469-18
25	68.5	7.1	295	3	US-08-651-136C-8
26	68.5	7.1	295	4	US-09-229-911A-8
27	68.5	7.1	877	1	US-08-072-574-12

28	68.5	7.1	877	1	US-08-486-270-12	Sequence 12, Appl
29	68.5	7.1	877	3	US-08-367-264-12	Sequence 12, Appl
30	68.5	7.1	877	4	US-09-153-757-12	Sequence 12, Appl
31	68.5	7.1	1180	1	US-08-072-574-8	Sequence 8, Appl
32	68.5	7.1	1180	1	US-08-486-270-8	Sequence 8, Appl
33	68.5	7.1	1180	3	US-08-367-264-8	Sequence 8, Appl
34	68.5	7.1	1180	4	US-09-153-757-8	Sequence 8, Appl
35	68.5	7.1	1212	1	US-08-072-574-10	Sequence 10, Appl
36	68.5	7.1	1212	1	US-08-486-270-10	Sequence 10, Appl
37	68.5	7.1	1212	3	US-08-367-264-10	Sequence 10, Appl
38	68.5	7.1	1212	4	US-09-153-757-10	Sequence 10, Appl
39	68	7.1	317	2	US-08-466-337A-18	Sequence 18, Appl
40	68	7.1	317	2	US-08-475-359-18	Sequence 18, Appl
41	68	7.1	317	3	US-08-465-887A-18	Sequence 18, Appl
42	67.5	7.0	178	1	US-08-825-891-1	Sequence 1, Appl
43	67.5	7.0	799	1	US-08-186-228-42	Sequence 42, Appl
44	67.5	7.0	799	1	US-08-332-638-42	Sequence 42, Appl
45	67	7.0	182	3	US-09-045-632-29	Sequence 29, Appl

ALIGNMENTS

RESULT 1
US-08-357-642A-1
; Sequence 1, Application US/08357642A
; Patent No. 5837524
; GENERAL INFORMATION:
; APPLICANT: Joseph Schlessinger
; APPLICANT: Sima Lev
; TITLE OF INVENTION: PYR2 RELATED PRODUCTS
; TITLE OF INVENTION: AND METHODS
; NUMBER OF SEQUENCES: 16
; CORRESPONDENCE ADDRESS:
; ADDRESS: Lyon & Lyon
; STREET: 633 West Fifth Street
; STREET: Suite 4700
; CITY: Los Angeles
; STATE: California
; COUNTRY: U.S.A.
; ZIP: 90071-2066
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 MB
; MEDIUM TYPE: storage
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: IBM P.C. DOS 5.0
; SOFTWARE: Word Perfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/357,642A
; FILING DATE: December 15, 1994
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Warburg, Richard J
; REGISTRATION NUMBER: 32,327
; REFERENCE/DOCKET NUMBER: 209/070
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (213) 489-1600
; TELEFAX: (213) 955-0440
; TELEX: 67-3510
; INFORMATION FOR SEQ. ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1009
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-08-357-642A-1
; Query Match 8.2%; Score 79.5; DB 2; Length 1009;
; Best Local Similarity 32.1%; Pred. No. 2.5;

Matches 25; Conservative 9; Mismatches 29; Indels 15; Gaps 3;

OY 88 EFKNTGSGLLGMANIDLEKSR-----TGDELLIPRGLEYVECTCEDCIKSPKV 138
DB 249 KFFNT---LAGFANIDQFYRCELQGNNTIVDLVIGPKRGRLTSDAPKPTCLAEKQI 305
OY 139 DSDHCFPLPAMEGATIL 156
DB 306 RSTRCLPL---EBCOAVL 320

RESULT 2

US-08-460-626-1
; Sequence 1, Application US/08460626
; Patent No. 5937815
; GENERAL INFORMATION:
; APPLICANT: STMA LEV
; APPLICANT: JOSEPH SCHLESSINGER
; TITLE OF INVENTION: PK-2 RELATED PRODUCTS AND
; TITLE OF INVENTION: METHODS
; NUMBER OF SEQUENCES: 25
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Lyon & Lyon
; STREET: 633 West Fifth Street
; CITY: Suite 4700
; STATE: Los Angeles
; STATE: California
; COUNTRY: U.S.A.
; ZIP: 90071-2066
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" diskette, 1.44 MB
; MEDIUM TYPE: storage
; OPERATING SYSTEM: IBM P.C. DOS 5.0
; SOFTWARE: Word Perfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/460,626
; FILING DATE: June 2, 1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/357,642
; FILING DATE: December 15, 1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Wardburg, Richard J.
; REGISTRATION NUMBER: 32,327
; REFERENCE/DOCKET NUMBER: 211/121
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (213) 489-1600
; TELEFAX: (213) 955-0440
; TELEFAX: 67-3510
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1009
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-460-626-1

Query Match 8.28; Score 79.5; DB 2; Length 1009;
Best Local Similarity 32.18; Pred. No. 2.5;
Matches 25; Conservative 9; Mismatches 29; Indels 15; Gaps 3;

OY 88 EFKNTGSGLLGMANIDLEKSR-----TGDELLIPRGLEYVECTCEDCIKSPKV 138
DB 249 KFFNT---LAGFANIDQFYRCELQGNNTIVDLVIGPKRGRLTSDAPKPTCLAEKQI 305
OY 139 DSDHCFPLPAMEGATIL 156
DB 306 RSTRCLPL---EBCOAVL 320

RESULT 3

US-08-810-572A-2
; Sequence 2, Application US/08810572A
; Patent No. 5969102
; GENERAL INFORMATION:
; APPLICANT: Bram, Richard J.
; APPLICANT: von Bulow, Goltz
; TITLE OF INVENTION: A LYMPHOCYTE SURFACE RECEPTOR THAT BINDS
; TITLE OF INVENTION: CAML, NUCLEIC ACIDS ENCODING THE SAME AND METHODS OF USE
; NUMBER OF SEQUENCES: 11
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: David A. Jackson, Esq.
; STREET: 411 Hackensack Ave, Continental Plaza, 4th
; STREET: Floor
; CITY: Hackensack
; STATE: New Jersey
; COUNTRY: USA
; ZIP: 07601

COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/810,572A
; FILING DATE: 28-FEB-1997
; CLASSIFICATION: 536
; ATTORNEY/AGENT INFORMATION:
; NAME: Jackson Esq., David A.
; REGISTRATION NUMBER: 26,742
; REFERENCE/DOCKET NUMBER: 1340-1-007
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 201-343-1684
; TELEFAX: 201-487-5800
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 293 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; HYPOTHETICAL: NO
; FRAGMENT TYPE: N-terminal
; ORIGINAL SOURCE:
; ORGANISM: Homo sapiens
US-08-810-572A-2

Query Match 8.18; Score 78.5; DB 2; Length 293;
Best Local Similarity 19.98; Pred. No. 0.56;
Matches 41; Conservative 35; Mismatches 73; Indels 57; Gaps 10;

OY 8 GSONEYFSLHACIPOLRCSSNTPLTQORCMASYNVSGT--NAIIMTCLGLSLI 65
DB 34 CPEQYWDPLGTCMCKCTICNHOS-ORTCAACRSLSCKRGGKYDHLIDCISCASI 92
OY 66 I-----SLAVFLMFL-----LKRISSEPLKDEKNTGSGLLGMANIDLEKSR----- 107
DB 93 CGQHPKOCAYFCENKIRSPVNLPELRRORSCEVENNSDMSGR--YGLEHROSEASPLAP 151
OY 108 ---RTGDELLIPRG-----LETYVECTCEDCIKSPK-----KVD 139
DB 152 GKLSADYALVYSLIGLCICAVLCCPLVAVACFLKKRQDPCSCQD--NSRPROSPAKSS 209
OY 140 SDHCFPLPAMEGATILVTTKTDNYC 165
DB 210 QDH-----AMEAGSPVSTSPPEVETC 230

RESULT 4

US-09-290-333-2
; Sequence 2, Application US/09290333
; Patent No. 6316222
; GENERAL INFORMATION:


```

APPLICANT: Bram, Richard J.
von Bulow, Gott
TITLE OF INVENTION: A LYMPHOCYTE SURFACE RECEPTOR THAT BINDS
CAML, NUCLEIC ACIDS ENCODING THE SAME AND METHODS OF USE
THEREOF
NUMBER OF SEQUENCES: 11
CORRESPONDENCE ADDRESS:
ADDRESSEE: David A. Jackson, Esq.
STREET: 411 Hackensack Ave, Continental Plaza, 4th
Floor
CITY: Hackensack
STATE: New Jersey
COUNTRY: USA
ZIP: 07601
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/290,333
FILING DATE: 12-Apr-1999
CLASSIFICATION: <Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: Jackson Esq., David A.
REGISTRATION NUMBER: 26,742
REFERENCE/DOCKET NUMBER: 1440-1-007 PCT
TELECOMMUNICATION INFORMATION:
TELEPHONE: 201-487-5800
TELEFAX: 201-343-1684
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 293 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: NO
FRAGMENT TYPE: N-terminal
ORIGINAL SOURCE:
ORGANISM: Homo sapiens
SEQUENCE DESCRIPTION: SEQ ID NO: 2:
US-09-290-333-2
Query Match 8.1%; Score 78.5; DB 4; Length 293;
Best Local Similarity 19.9%; Pred. No. 0.56; 73; Indels 57; Gaps 10;
Matches 41; Conservative 35; Mismatches 35
QY 8 CSONEYFSLHACIFPCQLRCSNTPPTTCORYCNASTYNSVKGT--NAIIATGLSLI 65
|:|:| | | | | | | | | | | | | | | | | | | | | | | | |
Db 34 CPREOVWDLPLGTGNCCKTICNHQS-ORTCAAFCRSLSCRRGKGFVDHLRDCISCAI 92
QY 66 I-----SLAVFVLMFL-----LRKISSEPLKDEKNTGSGLLGMANIDLEKS----- 107
| | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 93 CGGHPQCAFCFCENKLRSPVNLPPELRRORSGEVENNSDNGR-YQGLERGSEASPALP 151
QY 108 ---RTGDEIILPRG-----LETVVECTCEDCIKSKP-----KYD 139
| | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 152 GLKISADQVALVSTLGLCLCAVLCCFLVAVACFLKRGKDPGSCQP--RSRPPSPAKSS 209
QY 140 SDHCFLPAMEGATLTVTTKNDVC 165
| | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 210 QDH-----AMEAGSPVSTSPPEVETC 230
RESULT 5
US-08-179-481-2
; Sequence 2, Application US/08179481
; Patent No. 5624816
; GENERAL INFORMATION:
; APPLICANT: CARABAY, KERMIT L.
; APPLICANT: CAROTHERS CARABAY, CORALIE A.
; APPLICANT: FREIGTEN, NEVIS L.

```

```

TITLE OF INVENTION: ONCOGENE PRODUCT LIGAND
NUMBER OF SEQUENCES: 125
CORRESPONDENCE ADDRESS:
ADDRESSEE: CUSHMAN, DARBY & CUSHMAN
STREET: 1100 NEW YORK AVENUE, N.W.
CITY: WASHINGTON
STATE: D.C.
COUNTRY: U.S.A.
ZIP: 20005-3918

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/179,481
FILING DATE: 28-DEC-1993
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/922,521
FILING DATE: 30-JUL-1992
ATTORNEY/AGENT INFORMATION:
NAME: KORULIS, PAUL N.
REGISTRATION NUMBER: 16,773
REFERENCE/DOCKET NUMBER: 200702/UM92-08CIP
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 861-3000
TELEFAX: (202) 822-0944
TELEX: 6714627 CUSH
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 744 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-179-481-2

Query Match      7.9%; Score 76; DB 1; Length 744;
Best Local Similarity 22.1%; Pred. No. 4.2;
Matches 34; Conservative 29; Mismatches 57; Indels 34; Gaps 6;

OY    4  MACGQNEVEFYSLHACIPCQLRCSSNTPPLTCORC-----NASVTNSVKGK 52
       :|::||:::||::||::||::||::||::||::||::||::||::||::||::||
Db    49  LEGRITQTSANANTNTIAPAQYNTSSLKSPTTQWFLPNDTRVVHNNOYAFTSOT 108
OY    53  NAI-LMTCLGLSL1-----ISLAVFMFLLRKISSSEPLKDEKFKTGSGLLG 98
       :::||::||::||::||::||::||::||::||::||::||::||::||
Db    109  EDLPFNAGCVLLDINGQSVAHFDPGTIVTISIALSNILHASS--LSEERYRHHTGILL 166
OY    99  MANIDLEKSRNGDEITLPGLGYEDVECTCECKI 132
       :|::||::||::||::||::||::||::||::||::||::||::||
Db    167  VMNDNPE----DDFRMPNG--SIIPSNTSETL 193

RESULT 6
US-07-717-331F-2
: Sequence 32, Application US/07717331F
: Patent No. 5484905
GENERAL INFORMATION:
APPLICANT: June Nasrallah; Michael Nasrallah; and Joshua
APPLICANT: Stein
TITLE OF INVENTION: A Receptor Protein Kinase Gene
NUMBER OF INVENTION: Encoded At The Self-Incompatibility Locus
NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESSES:
ADDRESSEE: Yahwak & Associates
STREET: 25 Skytop Drive
CITY: Trumbull
STATE: Connecticut
COUNTRY: USA
ZIP: 06611
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy Disk
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COMPUTER: Macintosh
OPERATING SYSTEM: MS-DOS
SOFTWARE: Microsoft Word
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/717.331F
FILING DATE: June 19th 1991
CLASSIFICATION: 800
ATTORNEY/AGENT INFORMATION:
NAME: George M. Yahwak
REGISTRATION NUMBER: 26,824
TELECOMMUNICATION INFORMATION:
TELEPHONE: (203)268-1951
TELEFAX: (203)268-1951
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 857 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-07-717-331F-2

Query Match 7.8%; Score 75; DB 1; Length 857;
Best Local Similarity 17.6%; Pred. No. 6.6;
Matches 33; Conservative 30; Mismatches 50; Indels 74; Gaps 7;

QY 24 COLRCSSNTPPLTCORCNASVTNSVKGTNAIIMT-----58
DB 380 CKRRCISD--CNCFAFANADIRNG--GSGCVIMTERLEDIRNATDAIDGDLVYRLAA 434
QY 59 -----CLGLSLIILAVFLVLMFLRKISSEPLKDEFKNGSGILGMANIDLEK 106
DB 435 ADIAKRNASGKIISLTGVSVLLILINFCL-----WKRKOKRAKASISIANQRNQ 487
QY 107 SRIGDIIIPRLETTYEECTCEGDKSKPKVSDHCF-----PLPAMEGATILVTYT 161
DB 488 NUPNEMVLI-----SSKREFSGEYKFEELPLEIME---TVKATFN 527
QY 162 NDYCKSL 168
DB 528 FSSCKNL 534

RESULT 7
US-09-232-160-18
Sequence 18, Application US/09232160
Patent No. 6368794
GENERAL INFORMATION:
APPLICANT: Steve Daniel
APPLICANT: James Gilmore
APPLICANT: Susan G. Stuart
APPLICANT: Laura Stuve
TITLE OF INVENTION: DETECTION OF ALTERED EXPRESSION OF GENES REGULATING CELL
FILE OF INVENTION: PROLIFERATION
FILE REFERENCE: PA-0003 US
CURRENT APPLICATION NUMBER: US/09/232.160
CURRENT FILING DATE: 1999-01-15
NUMBER OF SEQ ID NOS: 23
SOFTWARE: PERL Program
SEQ ID NO 18
LENGTH: 134
TYPE: PRT
ORGANISM: Homo sapiens
FEATURE:
OTHER INFORMATION: 1299627
US-09-232-160-18

Query Match 7.3%; Score 70.5; DB 4; Length 154;
Best Local Similarity 25.2%; Pred. No. 1.9;
Matches 30; Conservative 16; Mismatches 52; Indels 21; Gaps 6;
QY 13 YFDSLIIHAC-IPCOLRCSSNTPPLTCORCNASVTNSVKGTNAIIMTCLG-----LSLIS 67
DB 23 YADDLAQCGKDKSKYCCDGTTPYCCSY--ATIGNILSGT-AIAGIVGVETIAGVIAG 79

QY 68 LAVFVLMFLRKISSEPLKDEFKNGSGILGMANIDLEKSRGTDEIILPRLETTYVEC 126
DB 80 IALICMCM-----KNHRATRVGILRTTHINTVSSYPGP---PYGHDEMEYC 125

RESULT 8
US-08-810-572A-6
Sequence 6, Application US/08810572A
Patent No. 5969102
GENERAL INFORMATION:
APPLICANT: Bram, Richard J.
APPLICANT: von Bulow, Goltz
TITLE OF INVENTION: A LYMPHOCYTE SURFACE RECEPTOR THAT BINDS
TITLE OF INVENTION: CAML, NUCLEIC ACIDS ENCODING THE SAME AND METHODS OF USE
NUMBER OF SEQUENCES: 11
CORRESPONDENCE ADDRESS:
ADDRESSER: David A. Jackson, Esq.
STREET: 411 Hackensack Ave, Continental Plaza, 4th
STREET: Floor
CITY: Hackensack
STATE: New Jersey
COUNTRY: USA
ZIP: 07601
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/810.572A
FILING DATE: 28-FEB-1997
CLASSIFICATION: 536
ATTORNEY/AGENT INFORMATION:
NAME: Jackson Esq., David A.
REGISTRATION NUMBER: 26,742
REFERENCE/DOCKET NUMBER: 1340-1-007
TELECOMMUNICATION INFORMATION:
TELEPHONE: 201-487-5800
TELEFAX: 201-343-1684
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 166 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
HYPOTHETICAL: NO
FRAGMENT TYPE: N-terminal
ORIGINAL SOURCE:
ORGANISM: Homo sapiens
US-08-810-572A-6

Query Match 7.2%; Score 69.5; DB 2; Length 166;
Best Local Similarity 25.0%; Pred. No. 2.8;
Matches 15; Conservative 14; Mismatches 28; Indels 3; Gaps 2;
QY 8 CSONEYPSLIIHACIPCOLRCSSNTPPLTCORCNASVTNSVGT--NAIIMTCLGLSLI 65
DB 34 CPEDYWPDLITCKSKCTTICNHOS-ORTCAFCRSLSCKEKGKRYDHLIDICISASI 92

RESULT 9
US-09-290-333-6
Sequence 6, Application US/09290333
Patent No. 6316222
GENERAL INFORMATION:
APPLICANT: Bram, Richard J.
APPLICANT: von Bulow, Goltz
TITLE OF INVENTION: A LYMPHOCYTE SURFACE RECEPTOR THAT BINDS
CAML, NUCLEIC ACIDS ENCODING THE SAME AND METHODS OF USE
THEREOF

NUMBER OF SEQUENCES: 11
CORRESPONDENCE ADDRESS:
ADDRESSEE: David A. Jackson, Esq.
STREET: 411 Hackensack Ave, Continental Plaza, 4th
Floor
CITY: Hackensack
STATE: New Jersey
COUNTRY: USA
ZIP: 07601
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/290,333
FILING DATE: 12-Apr-1999
CLASSIFICATION: <Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: Jackson Esq., David A.
REGISTRATION NUMBER: 26,742
REFERENCE/DOCKET NUMBER: 1340-1-007 PCT
TELECOMMUNICATION INFORMATION:
TELEPHONE: 201-487-5800
TELEFAX: 201-343-1684
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 166 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
HYPOTHETICAL: NO
FRAGMENT TYPE: N-terminal
ORIGINAL SOURCE:
ORGANISM: Homo sapiens
SEQUENCE DESCRIPTION: SEQ ID NO: 6:
US-09-290-333-6
Query Match 7.2%; Score 69.5; DB 4; Length 166;
Best Local Similarity 25.0%; Pred. No. 2.8;
Matches 15; Conservative 14; Mismatches 28; Indels 3; Gaps 2;
QY 8 CSONEYFDSLHACIPQCRSSNTPPTQRCYCNASVTSVKGT--NALIMTCLGISLI 65
Db 34 CPBQYWDPLIGTCMCKRTICNHQS-QRTCAFCRSLSCREKGFYDHLIDICISASI 92
RESULT 10
US-08-660-148-2
Sequence 2, Application US/08660148
Patent No. 6211353
GENERAL INFORMATION:
APPLICANT: Burnett, J. P.
APPLICANT: Mayne, Nancy G.
APPLICANT: Sharp, Robert L.
APPLICANT: Snyder, Yvonne M.
TITLE OF INVENTION: EXCITATORY AMINO RECEPTOR PROTEIN AND
TITLE OF INVENTION: RELATED NUCLEIC ACID COMPOUNDS
NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
ADDRESSEE: Eli Lilly and Company
STREET: Lilly Corporate Center
CITY: Indianapolis
STATE: Indiana
COUNTRY: United States of America
ZIP: 46285
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/660,148
FILING DATE:
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Gaylo, Paul J.
REGISTRATION NUMBER: 36,808
REFERENCE/DOCKET NUMBER: X-9419
TELECOMMUNICATION INFORMATION:
TELEPHONE: (317) 276-0756
TELEFAX: (317) 276-3861
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 1180 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-660-148-2
Query Match 7.2%; Score 69.5; DB 4; Length 1180;
Best Local Similarity 24.6%; Pred. No. 46;
Matches 49; Conservative 21; Mismatches 52; Indels 77; Gaps 14;

APPLICATION NUMBER: US/08/660,148
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/282,853
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Gaylo, Paul J.
REGISTRATION NUMBER: 36,808
REFERENCE/DOCKET NUMBER: X-9419
TELECOMMUNICATION INFORMATION:
TELEPHONE: (317) 276-0756
TELEFAX: (317) 276-3861
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 1180 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-660-148-2
Query Match 7.2%; Score 69.5; DB 4; Length 1180;
Best Local Similarity 24.6%; Pred. No. 46;
Matches 49; Conservative 21; Mismatches 52; Indels 77; Gaps 14;
QY 8 CSONEY-FDSLHACIPQCRSSNTPPTQRCYCNASVTSVKGTN----AILMTCLG 61
Db 537 KENEYVFDE--YTCRACOLG-SWPTDILT--GCDLIPVOYLHMGDEPIAAVFACLG 590
QY 62 LSLISLAVFVLMFLR-----KISSEPLKDEFKNTGSGLLGMNIDLEKSRIDEIILP 116
Db 591 --LNLTFVTVVFLIIRDPYVKSSREL-----YIIL 622
QY 117 RLEYIVIEEC--TCEDCIKSKPKYDSHCF-----PLPAMEGATILVTKTN--- 162
Db 623 AGI-----CLGYLCFTCLAKPK--QIYCYLQRIIGILSPAMSYSAIV--TETNRIAR 671
QY 163 -----DYCKSLPALISA 174
Db 672 ILASGKKIKTKKPKRPSA 690
RESULT 11
US-08-660-148-5
Sequence 5, Application US/08660148
Patent No. 6211353
GENERAL INFORMATION:
APPLICANT: Burnett, J. P.
APPLICANT: Mayne, Nancy G.
APPLICANT: Sharp, Robert L.
APPLICANT: Snyder, Yvonne M.
TITLE OF INVENTION: EXCITATORY AMINO RECEPTOR PROTEIN AND
TITLE OF INVENTION: RELATED NUCLEIC ACID COMPOUNDS
NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
ADDRESSEE: Eli Lilly and Company
STREET: Lilly Corporate Center
CITY: Indianapolis
STATE: Indiana
COUNTRY: United States of America
ZIP: 46285
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/660,148
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/282,853
FILING DATE:

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ATTORNEY/AGENT INFORMATION:
NAME: Gaylo, Paul J.
REGISTRATION NUMBER: 36,808
REFERENCE/DOCKET NUMBER: X-9419
TELECOMMUNICATION INFORMATION:
TELEPHONE: (317) 276-0756
TELEFAX: (317) 276-3861
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 1212 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-660-148-5

Query Match
Best Local Similarity 7.2%; Score 69.5; DB 4; Length 1212;
24.6%; Pred. No. 47;
Matches 49; Conservative 21; Mismatches 52; Indels 77; Gaps 14;

QY 8 CSQNER-FPSLHACIPCOLRCSSNTPL/TCORVCNASVTNSVKGTN-----AIIWTCIG 61
DB 537 CKNEVEFE--YTCRACQLG--SMPTDILT---GCDLIPVQYLKMGDPEPIAAVPAQLG 590
QY 62 LSLIISLAFLVFLRLR-----KISEPLKDFKNTGSGLLGMANIDLEKSRIGDEIILP 116
DB 591 --LLATLFTVVFIIYRDPYVKSSREL-----YITL 622
QY 117 RGLLEYVEEC---TEEDCIKSKPKVSDHCF-----PLPAMEGATIIIVTKTN---- 162
DB 623 AGI-----CLGYLCTFCLIAKPK--QIYCYLQRIIGLGLSPAMSYSLV---TKTNRIAR 671
QY 163 -----DYCKSLPAALSA 174
DB 672 ILAGSKKKICTKKKPRFMSA 690

RESULT 12
US-08-459-568-2
Sequence 2, Application US/08459568
Patent No. 5811304
GENERAL INFORMATION:
APPLICANT: Huang, Shi
TITLE OF INVENTION: Retinoblastoma Protein - Interacting
NUMBER OF SEQUENCES: 93
CORRESPONDENCE ADDRESS:
ADDRESS: Campbell and Flores
STREET: 4370 La Jolla Village Drive, Suite 700
CITY: San Diego
STATE: California
COUNTRY: USA
ZIP: 92122
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/459,568
FILING DATE: 02-JUN-1995
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/399,411
FILING DATE: 06-MAR-1995
ATTORNEY/AGENT INFORMATION:
NAME: Campbell, Cathryn A.
REGISTRATION NUMBER: 31,815
REFERENCE/DOCKET NUMBER: P-LJ 1264
TELECOMMUNICATION INFORMATION:
TELEPHONE: (619) 535-8949
TELEFAX: (619) 535-9001
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:

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LENGTH: 1706 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-459-568-2

Query Match
Best Local Similarity 7.2%; Score 69.5; DB 2; Length 1706;
21.7%; Pred. No. 77;
Matches 34; Conservative 22; Mismatches 44; Indels 57; Gaps 7;

QY 34 PLTCORVCNASVTNSVKGTNALLMTCLGLSLIISLAFLVFLRLRKISSEPLKDERKNTG 93
DB 598 PVTVE-----ITONIKSTOV-----SVTDLLKDSPPST- 626
QY 94 SGLLGMANIDLEKSRIGDEIILPRLLEYVEECTCEDCIKSKP-----KVDSDHCFPLP 147
DB 627 -----NCESKKRRTASPPVLPKIKTETESDSTAPSCSLPLSTIAVVSFFH----- 674
QY 148 AMEGATIIIVTKTNDYCK-----SLPAALSAETIER 179
DB 675 -KEKG--VYLSKMLQLODTQDKTLTPAGFSAAEIPK 708

RESULT 13
US-08-399-411-2
Sequence 2, Application US/08399411
Patent No. 5831008
GENERAL INFORMATION:
APPLICANT: Huang, Shi
TITLE OF INVENTION: Retinoblastoma Protein - Interacting
NUMBER OF SEQUENCES: 93
CORRESPONDENCE ADDRESS:
ADDRESS: Campbell and Flores
STREET: 4370 La Jolla Village Drive, Suite 700
CITY: San Diego
STATE: California
COUNTRY: USA
ZIP: 92122
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/399,411
FILING DATE: 06-MAR-1995
CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: Campbell, Cathryn A.
REGISTRATION NUMBER: 31,815
REFERENCE/DOCKET NUMBER: P-LJ 1264
TELECOMMUNICATION INFORMATION:
TELEPHONE: (619) 535-8949
TELEFAX: (619) 535-9001
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 1706 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-399-411-2

Query Match
Best Local Similarity 7.2%; Score 69.5; DB 2; Length 1706;
21.7%; Pred. No. 77;
Matches 34; Conservative 22; Mismatches 44; Indels 57; Gaps 7;

QY 34 PLTCORVCNASVTNSVKGTNALLMTCLGLSLIISLAFLVFLRLRKISSEPLKDERKNTG 93
DB 598 PVTVE-----ITONIKSTOV-----SVTDLLKDSPPST- 626
QY 94 SGLLGMANIDLEKSRIGDEIILPRLLEYVEECTCEDCIKSKP-----KVDSDHCFPLP 147
DB 627 -----NCESKKRRTASPPVLPKIKTETESDSTAPSCSLPLSTIAVVSFFH----- 674
QY 148 AMEGATIIIVTKTNDYCK-----SLPAALSAETIER 179
DB 675 -KEKG--VYLSKMLQLODTQDKTLTPAGFSAAEIPK 708

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Db 627 -----NCSKRRRTASPVLPKITESTESSTAPSCSLPLSISTAEVVSFH----- 674
 Oy 148 AMEGATILVTTKNDYCK-----SLPALSTATEIK 179
 Db 675 -KEGG-VYLSKLLKOLLQOTODKLTLPAGSAAEIPK 708

RESULT 14

US-08-516-859A-2
 Sequence 2, Application US/08516859A
 Patent No. 6069231
 GENERAL INFORMATION:
 APPLICANT: Huang, Shi
 TITLE OF INVENTION: Retinoblastoma Protein - Interacting
 NUMBER OF SEQUENCES: 106
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Campbell & Flores LLP
 STREET: 4370 La Jolla Village Drive, Suite 700
 CITY: San Diego
 STATE: California
 COUNTRY: USA
 ZIP: 92122
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/516,859A
 FILING DATE: 18-AUG-1995
 CLASSIFICATION: 514
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 08/399,411
 FILING DATE: 06-MAR-1995
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 08/292,683
 FILING DATE: 18-AUG-1994
 ATTORNEY/AGENT INFORMATION:
 NAME: Campbell, Cathryn A.
 REGISTRATION NUMBER: 31,815
 REFERENCE/DOCKET NUMBER: P-LJ 1776
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (619) 535-9001
 TELEFAX: (619) 535-8949
 INFORMATION FOR SEQ ID NO: 2:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 1706 amino acids
 TYPE: amino acid
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 US-08-516-859A-2

Query Match 7.2%; Score 69.5; DB 3; Length 1706;
 Best Local Similarity 21.7%; Pred. No. 77;
 Matches 34; Conservative 22; Mismatches 44; Indels 57; Gaps 7;
 Oy 34 PLTCORVCNMSVTSVNGTNAIIMTCLGSLIISLAVFVLMFLKRISSSEPLKDEPKNTG 93
 Db 598 PVYVE-----ITONIKSTGV-----SVTDLLKDKSPSST- 626
 Oy 94 SGLGMANIDLEKSRGTDEIILPRGLETYVEECTCEDCIKSP-----KYDSHCFLPL 147
 Db 627 -----NCSKRRRTASPVLPKITESTESSTAPSCSLPLSISTAEVVSFH----- 674
 Oy 148 AMEGATILVTTKNDYCK-----SLPALSTATEIK 179
 Db 675 -KEGG-VYLSKLLKOLLQOTODKLTLPAGSAAEIPK 708

RESULT 15
 US-09-586-472-2
 Sequence 2, Application US/09586472

Patent No. 6323335
 GENERAL INFORMATION:
 APPLICANT: Huang, Shi
 TITLE OF INVENTION: Retinoblastoma Protein - Interacting
 NUMBER OF SEQUENCES: 106
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Campbell & Flores LLP
 STREET: 4370 La Jolla Village Drive, Suite 700
 CITY: San Diego
 STATE: California
 COUNTRY: USA
 ZIP: 92122
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/09/586,472
 FILING DATE: 01-Jun-2000
 CLASSIFICATION: <Unknown>
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 09/528,706
 FILING DATE: 17-MAR-2000
 APPLICATION NUMBER: US 08/516,859
 FILING DATE: 18-AUG-1995
 APPLICATION NUMBER: US 08/399,411
 FILING DATE: 06-MAR-1995
 APPLICATION NUMBER: US 08/292,683
 FILING DATE: 18-AUG-1994
 ATTORNEY/AGENT INFORMATION:
 NAME: Campbell, Cathryn A.
 REGISTRATION NUMBER: 31,815
 REFERENCE/DOCKET NUMBER: P-LJ 4130
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (619) 535-9001
 TELEFAX: (619) 535-8949
 INFORMATION FOR SEQ ID NO: 2:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 1706 amino acids
 TYPE: amino acid
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 SEQUENCE DESCRIPTION: SEQ ID NO: 2:
 US-09-586-472-2

Query Match 7.2%; Score 69.5; DB 4; Length 1706;
 Best Local Similarity 21.7%; Pred. No. 77;
 Matches 34; Conservative 22; Mismatches 44; Indels 57; Gaps 7;
 Oy 34 PLTCORVCNMSVTSVNGTNAIIMTCLGSLIISLAVFVLMFLKRISSSEPLKDEPKNTG 93
 Db 598 PVYVE-----ITONIKSTGV-----SVTDLLKDKSPSST- 626
 Oy 94 SGLGMANIDLEKSRGTDEIILPRGLETYVEECTCEDCIKSP-----KYDSHCFLPL 147
 Db 627 -----NCSKRRRTASPVLPKITESTESSTAPSCSLPLSISTAEVVSFH----- 674
 Oy 148 AMEGATILVTTKNDYCK-----SLPALSTATEIK 179
 Db 675 -KEGG-VYLSKLLKOLLQOTODKLTLPAGSAAEIPK 708

Search completed: November 12, 2002, 17:01:40
 Job time : 28.2704 secs

GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on: November 12, 2002, 17:00:26 ; Search time 14.2146 Seconds
(without alignments)
186,640 Million cell updates/sec

Title: US-09-848-271-2

Perfect score: 964

Sequence: 1 MLOMAGCCSNEYFDSLHA.....CKSLPALSTELKSTISAR 184

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 92612 seqs, 14418503 residues

Total number of hits satisfying chosen parameters: 92612

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 08

Maximum Match 1008

Listing first 45 summaries

Database : Published Applications AA:*

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	950	98.5	181	10	US-09-854-864-5 Sequence 5, Appl1
2	572	59.3	185	10	US-09-854-864-11 Sequence 11, Appl1
3	323	33.5	58	10	US-09-854-864-21 Sequence 21, Appl1
4	311.5	32.3	117	10	US-09-854-864-12 Sequence 12, Appl1
5	286	29.7	283	10	US-09-854-864-9 Sequence 9, Appl1
6	284	29.5	51	10	US-09-854-864-6 Sequence 6, Appl1
7	201	20.9	34	10	US-09-854-864-7 Sequence 7, Appl1
8	201	20.9	81	10	US-09-854-864-13 Sequence 13, Appl1
9	187	19.4	281	10	US-09-854-864-10 Sequence 10, Appl1
10	104	10.8	21	10	US-09-854-864-8 Sequence 8, Appl1
11	79.5	8.2	293	8	US-09-778-050A-42 Sequence 42, Appl1
12	79.5	8.2	1009	8	US-08-987-689A-2 Sequence 2, Appl1
13	78.5	8.1	293	10	US-09-879-919-22 Sequence 22, Appl1
14	78.5	8.1	293	10	US-09-854-864-14 Sequence 14, Appl1
15	78.5	8.1	293	10	US-09-961-376-2 Sequence 2, Appl1
16	78	8.1	291	9	US-09-779-050A-43 Sequence 43, Appl1
17	70.5	7.3	397	10	US-09-854-864-18 Sequence 18, Appl1
18	70.5	7.3	1203	12	US-10-027-923-5 Sequence 5, Appl1
19	70	7.3	180	10	US-09-780-717-11 Sequence 11, Appl1

20	70	7.3	182	10	US-09-780-717-44 Sequence 44, Appl1
21	70	7.3	836	10	US-09-925-301-1088 Sequence 1088, Appl1
22	69.5	7.2	59	10	US-09-854-864-20 Sequence 20, Appl1
23	69.5	7.2	166	10	US-09-854-864-15 Sequence 15, Appl1
24	69.5	7.2	1212	12	US-10-027-923-4 Sequence 4, Appl1
25	69	7.2	324	10	US-09-787-481-7 Sequence 7, Appl1
26	69	7.2	772	10	US-09-815-837-74 Sequence 74, Appl1
27	69	7.2	774	10	US-09-815-837-72 Sequence 72, Appl1
28	68.5	7.1	305	10	US-09-771-730-119 Sequence 119, Appl1
29	67.5	7.0	37	9	US-09-779-050A-45 Sequence 45, Appl1
30	67.5	7.0	664	10	US-09-780-525-2 Sequence 2, Appl1
31	67	7.0	320	10	US-09-797-481-8 Sequence 8, Appl1
32	67	7.0	1113	10	US-09-836-470B-3 Sequence 3, Appl1
33	66.5	6.9	67	10	US-09-854-864-16 Sequence 16, Appl1
34	66	6.8	317	9	US-09-844-988-1 Sequence 1, Appl1
35	66	6.8	317	10	US-09-844-908-1 Sequence 1, Appl1
36	66	6.8	376	10	US-09-735-787-4 Sequence 4, Appl1
37	65.5	6.8	728	12	US-09-908-322-2 Sequence 2, Appl1
38	65.5	6.8	798	12	US-10-078-929-192 Sequence 192, Appl1
39	65.5	6.8	3034	10	US-09-737-149-25 Sequence 25, Appl1
40	65.5	6.8	3034	10	US-09-737-149-30 Sequence 30, Appl1
41	65	6.7	386	12	US-10-039-785-4 Sequence 4, Appl1
42	65	6.7	386	12	US-10-105-929-6 Sequence 6, Appl1
43	64.5	6.7	195	10	US-09-005-243-44 Sequence 44, Appl1
44	64.5	6.7	195	10	US-09-224-683-44 Sequence 44, Appl1
45	64.5	6.7	418	9	US-09-886-429-2 Sequence 2, Appl1

ALIGNMENTS

RESULT 1

US-09-854-864-5
Sequence 5, Application US/09854864
Patent No. US20020081296A1
GENERAL INFORMATION:
APPLICANT: THELL, LARS EYDE
APPLICANT: VU, GANG
TITLE OF INVENTION: METHODS AND COMPOSITIONS OF MATTER CONCERNING APRIL/670, BCMA,
FILE REFERENCE: A-686B
CURRENT APPLICATION NUMBER: US/09/854, 864
CURRENT FILING DATE: 2001-09-11
PRIOR APPLICATION NUMBER: US 60/204,039
PRIOR FILING DATE: 2000-05-12
PRIOR APPLICATION NUMBER: US 60/214,591
PRIOR FILING DATE: 2000-06-27
NUMBER OF SEQ ID NOS: 31
SOFTWARE: PatentIn version 3.1
SEQ ID NO 5
LENGTH: 181
TYPE: PRT
ORGANISM: Homo sapiens
US-09-854-864-5

Query Match 98.5%; Score 950; DB 10; Length 181;

Best Local Similarity 100.0%; Pred. No. 2e-89;

Matches 181; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY	4	MAGCCSNEYFDSLHACIPCOLRCSNPPTTCORCNASVTSVSGTNAIILMTCTGLS 63			Sequence 44, Appl1
DB	1	MAGCCSNEYFDSLHACIPCOLRCSNPPTTCORCNASVTSVSGTNAIILMTCTGLS 60			Sequence 20, Appl1
QY	64	LIISLAFVLMFLIRKISSEPLKDEKRTNGSLGMANIDLEKSTGDEIILPGLGYTV 123			Sequence 15, Appl1
DB	61	LIISLAFVLMFLIRKISSEPLKDEKRTNGSLGMANIDLEKSTGDEIILPGLGYTV 120			Sequence 4, Appl1
QY	124	EECCCECISKRKVDSDHCFPLPAMEGATILVTTKNDYCKSLPALSTELKSTISA 183			Sequence 74, Appl1
DB	121	EECCCECISKRKVDSDHCFPLPAMEGATILVTTKNDYCKSLPALSTELKSTISA 180			Sequence 72, Appl1
QY	184	R 184			Sequence 45, Appl1

Db 181 R 181

RESULT 2
US-09-854-864-11

; Sequence 11, Application US/09854864

; Patent No. US20020081296A1

; GENERAL INFORMATION:

; APPLICANT: THEILL, LARS EYDE

; TITLE OF INVENTION: METHODS AND COMPOSITIONS OF MATTER CONCERNING APRIL/G70, BCMA,

; FILE REFERENCE: A-686B

; CURRENT APPLICATION NUMBER: US/09/854,864

; PRIOR APPLICATION NUMBER: US 60/204,039

; PRIOR FILING DATE: 2000-05-12

; PRIOR APPLICATION NUMBER: US 60/214,591

; PRIOR FILING DATE: 2000-06-27

; NUMBER OF SEQ ID NOS: 31

; SOFTWARE: PatentIn version 3.1

; SEQ ID NO 11

; LENGTH: 185

; TYPE: PRT

; ORGANISM: Murine

US-09-854-864-11

Query Match 59.3%; Score 572; DB 10; Length 185;
Best Local Similarity 62.6%; Pred. No. 4,8e-51;

Matches 117; Conservative 21; Mismatches 41; Indels 8; Gaps 4;

OY 4 MAGOCSEYFDSLHACIPQCRSSNTPLTCORNCASVTSVKTNAIIMTCLGLS 63

Db 1 MAOCSEYFDSLHACIPQCRSSNTPLTCORNCASVTSVKTNAIIMTCLGLS 58

OY 64 LIISLAVFLMLRKISSEPLKDEFKN---TSGGLGMANIDLEKSRGTDEIILPRGL 119

Db 59 LVLSLALFTTIFLKRKNPEALDKPQSGQLDSAGLDKADTELTRIRADDNRIFRSL 118

OY 120 EYVEECCECCIKSKPKYSDHCFPLPAMEGATILVTTKTDYCK-SLPAAL-SATEI 177

Db 119 EYVEECCECCIKSKPKYSDHCFPLPAMEGATILVTTKTDYCK-SLPAAL-SATEI 178

OY 178 EKSIAR 184

Db 179 EKPHTR 185

RESULT 3

US-09-854-864-21

; Sequence 21, Application US/09854864

; Patent No. US20020081296A1

; GENERAL INFORMATION:

; APPLICANT: THEILL, LARS EYDE

; TITLE OF INVENTION: METHODS AND COMPOSITIONS OF MATTER CONCERNING APRIL/G70, BCMA,

; FILE REFERENCE: A-686B

; CURRENT APPLICATION NUMBER: US/09/854,864

; PRIOR APPLICATION NUMBER: US 60/204,039

; PRIOR FILING DATE: 2000-05-12

; PRIOR APPLICATION NUMBER: US 60/214,591

; PRIOR FILING DATE: 2000-06-27

; NUMBER OF SEQ ID NOS: 31

; SOFTWARE: PatentIn version 3.1

; SEQ ID NO 21

; LENGTH: 58

; TYPE: PRT

; ORGANISM: Homo sapiens

US-09-854-864-21

Query Match 33.5%; Score 323; DB 10; Length 58;

Best Local Similarity 100.0%; Pred. No. 2,1e-26;
Matches 58; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 8 CSONEYFDSLHACIPQCRSSNTPLTCORNCASVTSVKTNAIIMTCLGLS 65

Db 1 CSONEYFDSLHACIPQCRSSNTPLTCORNCASVTSVKTNAIIMTCLGLS 58

RESULT 4

US-09-854-864-12

; Sequence 12, Application US/09854864

; Patent No. US20020081296A1

; GENERAL INFORMATION:

; APPLICANT: THEILL, LARS EYDE

; TITLE OF INVENTION: METHODS AND COMPOSITIONS OF MATTER CONCERNING APRIL/G70, BCMA,

; FILE REFERENCE: A-686B

; CURRENT APPLICATION NUMBER: US/09/854,864

; PRIOR APPLICATION NUMBER: US 60/204,039

; PRIOR FILING DATE: 2000-05-12

; PRIOR APPLICATION NUMBER: US 60/214,591

; PRIOR FILING DATE: 2000-06-27

; NUMBER OF SEQ ID NOS: 31

; SOFTWARE: PatentIn version 3.1

; SEQ ID NO 12

; LENGTH: 117

; TYPE: PRT

; ORGANISM: human-murine Consensus

US-09-854-864-12

Query Match 32.3%; Score 311.5; DB 10; Length 117;
Best Local Similarity 61.5%; Pred. No. 7,5e-25;

Matches 96; Conservative 4; Mismatches 7; Indels 49; Gaps 19;

OY 9 SONEYFDSLHACIPQCRSSNTPLTCORNCASVTSVKTNAIIMTCLGLS 68

Db 2 AOCSEYFDSLHACIPQCRSSNTPLTCORNCASVTSVKTNAIIMTCLGLS 43

OY 69 AVFLMFLRKISSEPLKDEFKN---TSGGLGMANIDLEKSRGTDEIILPRGL 128

Db 44 A-----FLKRL-----ELKDE-----GSLAL-----RD-----IPR-LEIVVECTC 76

OY 129 EDCIKSKPKYSDHCFPLPAMEGATILVTTKTDY 164

Db 77 EDC-KSKPK-DSDH-FPLPAMEGATILVTTKTDY 108

RESULT 5

US-09-854-864-9

; Sequence 9, Application US/09854864

; Patent No. US20020081296A1

; GENERAL INFORMATION:

; APPLICANT: THEILL, LARS EYDE

; TITLE OF INVENTION: METHODS AND COMPOSITIONS OF MATTER CONCERNING APRIL/G70, BCMA,

; FILE REFERENCE: A-686B

; CURRENT APPLICATION NUMBER: US/09/854,864

; PRIOR APPLICATION NUMBER: US 60/204,039

; PRIOR FILING DATE: 2000-05-12

; PRIOR APPLICATION NUMBER: US 60/214,591

; PRIOR FILING DATE: 2000-06-27

; NUMBER OF SEQ ID NOS: 31

; SOFTWARE: PatentIn version 3.1

; SEQ ID NO 9

; LENGTH: 283

; TYPE: PRT

; ORGANISM: Homo sapiens

US-09-854-864-9


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Query Match      29.5%; Score 284; DB 10; Length 51;
Best Local Similarity 100.0%; Pred. No. 1 6e-22;
Matches 51; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY      4 MAGCCSNEYFDSLHACIPCOLRCSSNTPPLTCORYCNASVMSVGKTN 54
|||||
Db       1 MAGCCSNEYFDSLHACIPCOLRCSSNTPPLTCORYCNASVMSVGKTN 51
|||||

RESULT 7
US-09-854-864-7
; Sequence 7, Application US/09854864
; Patent No. US20020081296A1
; GENERAL INFORMATION:
; APPLICANT: THEILL, LARS EYDE
; APPLICANT: YU, GANG
; TITLE OF INVENTION: METHODS AND COMPOSITIONS OF MATTER CONCERNING APRIL/G70, BCMA
; TITLE OF INVENTION: BLXS/AGP-3, AND TNCI
; FILE REFERENCE: A-686B
; CURRENT APPLICATION NUMBER: US/09/854,864
; CURRENT FILING DATE: 2001-09-11
; PRIOR APPLICATION NUMBER: US 60/204,039
; PRIOR FILING DATE: 2000-05-12
; PRIOR APPLICATION NUMBER: US 60/214,591
; PRIOR FILING DATE: 2000-06-27
; NUMBER OF SEQ ID NOS: 31
; SOFTWARE: Patentin version 3.1
; SEQ ID NO 7
```

Query Match	19.48;	Score 187;	DB 10;	Length 281;
Best Local Similarity	29.88;	Pred. NO. 9.8e-12;		

Matches 64: Conservative 17; Mismatches 54; Indels 80; Gaps 8;
QY 4 MAGGCSQNEYEDSLHACIPQOLRCSNTPTLCQRYCMASTNSYKGTNALMTCLGLS 63
1 MAAQCFHEBYEDSLHACIPQOLRCSNTPTLCQRYCMASTNSYKGTNALMTCLGLS 47
QY 64 LIISLAVFLMLFKLISSEPLKDEFNTGSG-----LLGMANIDLEKSR 108
48 -----YTGSGGDKHTHCPCPAPELLGSPVLFPPK 80
QY 109 TDEEILRLGLEYEECTCEDCKSKPKKDS-----HCFPLPAME-----CAT 154
DB 81 PBDTLMISRTBEVT---CVVVDVSHEDPEVKFMWYDGVGVHNAKTRPEQYNSYRNV 137
QY 155 ILVTTKTDY-----CKSLPALSATETIEKSI 182
DB 138 SVLTIVLHQDMLNGKRYCKVSNKALPA-PIEKITIS 171

RESULT 10

US-09-854-864-8
; Sequence 8, Application US/09854864
; Patent No. US20020081296A1
; GENERAL INFORMATION:
; APPLICANT: THEITL, IARS EYDE
; APPLICANT: YU, GANG
; TITLE OF INVENTION: METHODS AND COMPOSITIONS OF MATTER CONCERNING APRIL/G70, BCMA,
; TITLE OF INVENTION: BLTS/AGP-3, AND TACI
; FILE REFERENCE: A-6868
; CURRENT APPLICATION NUMBER: US/09/854,864
; CURRENT FILING DATE: 2001-09-11
; PRIOR APPLICATION NUMBER: US 60/204,039
; PRIOR FILING DATE: 2000-05-12
; PRIOR APPLICATION NUMBER: US 60/214,591
; PRIOR FILING DATE: 2000-06-27
; NUMBER OF SEQ ID NOS: 31
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 8
; LENGTH: 21
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-854-864-8

Query Match 10.8%; Score 104; DB 10; Length 21;

Best Local Similarity 100.0%; Pred. No. 0.0001;
Matches 21: Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 55 ILMTCLGLSLIISLAVFLMLF 75
DB 1 ILMTCLGLSLIISLAVFLMLF 21

RESULT 11

US-09-779-050A-42
; Sequence 42, Application US/09779050A
; Patent No. US20020160416A1
; GENERAL INFORMATION:
; APPLICANT: BOYLE, WILLIAM
; APPLICANT: HSU, HAILING
; TITLE OF INVENTION: RECEPTOR FROM TNF FAMILY
; FILE REFERENCE: A-5708
; CURRENT APPLICATION NUMBER: US/09/779,050A
; CURRENT FILING DATE: 2001-02-12
; PRIOR APPLICATION NUMBER: 60/181,800
; PRIOR FILING DATE: 2000-02-11
; NUMBER OF SEQ ID NOS: 52
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 42
; LENGTH: 293
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-779-050A-42

Query Match 8.2%; Score 79.5; DB 9; Length 293;
Best Local Similarity 19.9%; Pred. No. 0.85;
Matches 41: Conservative 35; Mismatches 73; Indels 57; Gaps 10;

QY 8 CSQNEYPSLSLHACIPQOLRCSNTPTLCQRYCMASTNSYKGT--NALMTCLGLSLI 65
1 CSQNEYPSLSLHACIPQOLRCSNTPTLCQRYCMASTNSYKGT--NALMTCLGLSLI 65
DB 34 CPEQYMDPLLTGCMSCVTCINHO--QRTCAFCRSLSCKRKGKRYDHLMDICASCI 92
QY 66 I-----SLAVFLMLF-----LTKISSEPLKDEFNTGSGLLGMANIDLEKSR 107
DB 93 CGQHPKQAYFCENKLSFVNLPELNRORSGEVENSQSGR-YGLEHRSSEASPLP 151
QY 108 ---RTDEEILRLGLEYEECTCEDCKSKPKKDS-----HCFPLPAME-----CAT 139
DB 152 GKLSADQVALVYVSTGLCLCAVLCCFLVAVACFLKMRDPCSCGP--RSRPQSPAKSS 209
QY 140 SDHCPLPAMEGATILVTTKTDY 165
DB 210 QDH-----AMEKGSVSTSPPEVETC 230

RESULT 12

US-08-987-689A-2
; Sequence 2, Application US/08987689A
; Patent No. US20020048782A1
; GENERAL INFORMATION:
; APPLICANT: Sima Ley
; APPLICANT: Joseph Schlessinger
; TITLE OF INVENTION: PK2 RELATED PRODUCTS AND METHODS
; NUMBER OF SEQUENCES: 32
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Lyon & Lyon
; STREET: 633 West Fifth Street
; CITY: Los Angeles
; STATE: California
; COUNTRY: USA
; ZIP: 90071
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 MB storage
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: IBM P.C. DOS 5.0
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/987,689A
; FILING DATE: December 9, 1997
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/032,824
; FILING DATE: December 11, 1996
; APPLICATION NUMBER: 08/460,626
; FILING DATE: June 2, 1995
; APPLICATION NUMBER: 08/357,642
; FILING DATE: December 15, 1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Wardburg, Richard J.
; REGISTRATION NUMBER: 32,327
; REFERENCE/DOCKET NUMBER: 230/110
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (213) 489-1600
; TELEFAX: (213) 955-0440
; TELEX: 67-3510
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1009
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-987-689A-2

Query Match 8.2%; Score 79.5; DB 8; Length 1009;
Best Local Similarity 32.1%; Pred. No. 4;
Matches 25: Conservative 9; Mismatches 29; Indels 15; Gaps 3;

```
OY 88 EKNKTSGLLMANIDLEKSR-----TGDELLPRGLETYVECTCEDCIKSKRV 138
: 11 : 111111 : 111111 :
DB 249 KFEFN---LAFGANIDETRCCELLQGMNITVLYGPGIKQLTSQAKRPTCLAEFRKI 305
: 11 : 111111 : 111111 :
OY 139 DSDHCFLPAMEGATIL 156
: 11 : 111111 : 111111 :
DB 306 RSIRCLPL---EGGAVL 320

RESULT 13
US-09-879-919-22
: Sequence 22, Application US/09879919
: Patent No. US20020064829A1
: GENERAL INFORMATION:
: APPLICANT: Yu, Guo-Liang, et al.
: TITLE OF INVENTION: Human Tumor Necrosis Factor Delta and Epsilon
: FILE REFERENCE: PF253P1
: CURRENT APPLICATION NUMBER: US/09/879,919
: CURRENT FILING DATE: 2001-06-14
: PRIOR APPLICATION NUMBER: 60/293,499
: PRIOR FILING DATE: 2001-05-25
: PRIOR APPLICATION NUMBER: 60/277,978
: PRIOR FILING DATE: 2001-03-23
: PRIOR APPLICATION NUMBER: 60/276,248
: PRIOR FILING DATE: 2001-03-16
: PRIOR APPLICATION NUMBER: 60/254,875
: PRIOR FILING DATE: 2000-12-13
: PRIOR APPLICATION NUMBER: 60/241,952
: PRIOR FILING DATE: 2000-10-23
: PRIOR APPLICATION NUMBER: 60/211,537
: PRIOR FILING DATE: 2000-06-15
: PRIOR APPLICATION NUMBER: 08/815,783
: PRIOR FILING DATE: 1997-03-12
: PRIOR APPLICATION NUMBER: 60/016,812
: PRIOR FILING DATE: 1996-03-14
: NUMBER OF SEQ ID NOS: 26
: SOFTWARE: PatentIn Ver. 2.1
: SEQ ID NO 22
: LENGTH: 293
: TYPE: PRT
: ORGANISM: Homo sapiens
US-09-879-919-22

Query Match 8.1%; Score 78.5; DB 10; Length 293;
Best Local Similarity 19.9%; Pred. No. 1.1;
Matches 41; Conservative 35; Mismatches 73; Indels 57; Gaps 10;

OY 8 CSONEYFDSLHACIPCOLRCSNTPPLTCQRYCNASVTNSVKG---NAILMTCGLSLI 65
: 11 : 111111 : 111111 :
DB 34 CPEEQYWPDLGTCSCKTICNHQS-ORTCAAFCRSLSCRKEGKRYDHLRDCISCASI 92
: 11 : 111111 : 111111 :
OY 66 I-----SLAVFVLMFL-----LKRISSEPLKDEFNKTSGLLMANIDLEKSR----- 107
: 11 : 111111 : 111111 :
DB 93 CGQHKQCAFCECNKLRSPVNLPELRRORSGEVNNNSQSR-YQGLEHRSSEASPALP 151
: 11 : 111111 : 111111 :
OY 108 ---RTGDELLPRG-----LEVTVECTCEDCIKSKP-----KYD 139
: 11 : 111111 : 111111 :
DB 152 GLKLSADQVALVYSTLGICLCVLCFLVAVACFLKRRDPCSCQP--RSRRSPASS 209
: 11 : 111111 : 111111 :
OY 140 SDHCFLPAMEGATILVTTKTNDYC 165
: 11 : 111111 : 111111 :
DB 210 QDH-----AMEGSPVSTSPPEVETC 230
: 11 : 111111 : 111111 :

RESULT 14
US-09-854-864-14
: Sequence 14, Application US/09854864
: Patent No. US20020081296A1
: GENERAL INFORMATION:
: APPLICANT: THEILL, LARS EYDE
: APPLICANT: YU, GANG
: TITLE OF INVENTION: METHODS AND COMPOSITIONS OF MATTER CONCERNING APRIL/G70, BCMA,
```

```
: TITLE OF INVENTION: BLKS/AGP-3, AND TACTI
: FILE REFERENCE: A-6868
: CURRENT APPLICATION NUMBER: US/09/854,864
: CURRENT FILING DATE: 2001-09-11
: PRIOR APPLICATION NUMBER: US 60/204,039
: PRIOR FILING DATE: 2000-05-12
: PRIOR APPLICATION NUMBER: US 60/214,591
: PRIOR FILING DATE: 2000-06-27
: NUMBER OF SEQ ID NOS: 31
: SOFTWARE: PatentIn version 3.1
: SEQ ID NO 14
: LENGTH: 293
: TYPE: PRT
: ORGANISM: Homo sapiens
US-09-854-864-14

Query Match 8.1%; Score 78.5; DB 10; Length 293;
Best Local Similarity 19.9%; Pred. No. 1.1;
Matches 41; Conservative 35; Mismatches 73; Indels 57; Gaps 10;

OY 8 CSONEYFDSLHACIPCOLRCSNTPPLTCQRYCNASVTNSVKG---NAILMTCGLSLI 65
: 11 : 111111 : 111111 :
DB 34 CPEEQYWPDLGTCSCKTICNHQS-ORTCAAFCRSLSCRKEGKRYDHLRDCISCASI 92
: 11 : 111111 : 111111 :
OY 66 I-----SLAVFVLMFL-----LKRISSEPLKDEFNKTSGLLMANIDLEKSR----- 107
: 11 : 111111 : 111111 :
DB 93 CGQHKQCAFCECNKLRSPVNLPELRRORSGEVNNNSQSR-YQGLEHRSSEASPALP 151
: 11 : 111111 : 111111 :
OY 108 ---RTGDELLPRG-----LEVTVECTCEDCIKSKP-----KYD 139
: 11 : 111111 : 111111 :
DB 152 GLKLSADQVALVYSTLGICLCVLCFLVAVACFLKRRDPCSCQP--RSRRSPASS 209
: 11 : 111111 : 111111 :
OY 140 SDHCFLPAMEGATILVTTKTNDYC 165
: 11 : 111111 : 111111 :
DB 210 QDH-----AMEGSPVSTSPPEVETC 230
: 11 : 111111 : 111111 :

RESULT 15
US-09-961-376-2
: Sequence 2, Application US/09961376
: Patent No. US20020106736A1
: GENERAL INFORMATION:
: APPLICANT: Ruben et al.
: TITLE OF INVENTION: Human Tumor Necrosis Factor Receptor TR17
: FILE REFERENCE: PF524P1
: CURRENT APPLICATION NUMBER: US/09/961,376
: CURRENT FILING DATE: 2001-09-25
: PRIOR APPLICATION NUMBER: 60/254,874
: PRIOR FILING DATE: 2000-12-13
: PRIOR APPLICATION NUMBER: 60/235,991
: PRIOR FILING DATE: 2000-09-26
: PRIOR APPLICATION NUMBER: 09/533,822
: PRIOR FILING DATE: 2000-03-24
: PRIOR APPLICATION NUMBER: 60/188,208
: PRIOR FILING DATE: 2000-03-10
: NUMBER OF SEQ ID NOS: 7
: SOFTWARE: PatentIn Ver. 2.1
: SEQ ID NO 2
: LENGTH: 293
: TYPE: PRT
: ORGANISM: Homo sapiens
US-09-961-376-2

Query Match 8.1%; Score 78.5; DB 10; Length 293;
Best Local Similarity 19.9%; Pred. No. 1.1;
Matches 41; Conservative 35; Mismatches 73; Indels 57; Gaps 10;

OY 8 CSONEYFDSLHACIPCOLRCSNTPPLTCQRYCNASVTNSVKG---NAILMTCGLSLI 65
: 11 : 111111 : 111111 :
DB 34 CPEEQYWPDLGTCSCKTICNHQS-ORTCAAFCRSLSCRKEGKRYDHLRDCISCASI 92
: 11 : 111111 : 111111 :
OY 66 I-----SLAVFVLMFL-----LKRISSEPLKDEFNKTSGLLMANIDLEKSR----- 107
: 11 : 111111 : 111111 :
```

```

Db      93  CGQHPRQCAVPCENKLRSPVNI/PELRRQRSGEVENNSDNGR-YQGLEHRGSEASPALP 151
QY      108  ----RTGDEIILPRG-----LETVTECTGDCIKSKP-----KYD 139
Db      152  GLKLSADQVALYSTLGICLCAVLCCFLVAVACFLKKRGDPCSCQP--RSRPRQSPAKSS 209
QY      140  SDHCFFLPAMEGATILVTTKTNDYC 165
Db      210  QDH-----AMFAGSPVSTSPPEVETC 230

```

Search completed: November 12, 2002, 17:09:11
 Job time : 15.2146 secs

GenCore version 5.1.3
Copyright (c) 1993 - 2002 Compugen Ltd.

OM protein - protein search, using sw model

Run on: November 12, 2002, 16:56:36 ; Search time 28.4292 Seconds
(without alignments)
622.203 Million cell updates/sec

Title: US-09-848-271-2

Perfect score: 964

Sequence: 1 MLOMAGCCSONEYFDSLHA.....CKSLPALSAATEIKSISAR 184

Scoring table:

Gapop 10.0 , Gapext 0.5

Searched: 283224 seqs, 96134422 residues

Total number of hits satisfying chosen parameters: 283224

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database :

1: PIR.73:*
2: PIR1:*
3: PIR3:*
4: PIR4:*

Pred. NO. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	964	100.0	184	2	S43486 B-cell maturation
2	88.5	9.2	217	2	C97344 amino acid ABC tra
3	86.5	9.0	858	2	T08881 promilin - mouse
4	83.5	8.7	1998	2	T13009 hypothetical prote
5	82	8.5	1009	2	A57434 protein-tyrosine k
6	81.5	8.5	2233	2	T28669 surfact protein 51
7	81	8.4	773	2	D89010 protein-R08f11.7
8	79.5	8.2	1009	2	S60248 protein-tyrosine k
9	79.5	8.2	1299	2	T43251 furin (EC 3.4.21.7
10	78.5	8.1	343	2	D64469 protein-tyrosine k
11	78	8.1	841	2	JC5894 killer cell inhibi
12	77.5	8.0	738	2	D86345 hypothetical prote
13	77.5	8.0	968	2	T01733 hypothetical prote
14	77	8.0	522	2	T45824 hypothetical prote
15	76.5	7.9	539	2	T21152 methyl-accepting c
16	76.5	7.9	357	2	T21152 hypothetical prote
17	76.5	7.9	1404	2	T19277 asctes slatoglyco
18	76	7.9	744	2	A43353 complex I interned
19	76	7.9	748	2	T47250 probable transcrip
20	75.5	7.8	638	2	T41478 hydroxylase chain
21	75	7.8	450	2	B97297 S-receptor kinase
22	75	7.8	857	1	A41369 ERD1 protein - yea
23	74.5	7.7	384	2	S45392 hypothetical prote
24	74.5	7.7	1101	2	T16840 chitinase (EC 3.2.
25	74	7.7	377	2	JC7535 conserved hypothet
26	73.5	7.6	307	2	B95099 hypothetical prote
27	73.5	7.6	307	2	A97967 protein F20N2.12
28	73	7.6	304	2	A89882
29	73	7.6	679	2	B96599

30	73	7.6	733	1	A46373 probable setine/th
31	72.5	7.5	243	2	T31144 hypothetical prote
32	72.5	7.5	408	2	B84518 hypothetical prote
33	72	7.5	416	2	S75097 hypothetical prote
34	72	7.5	855	2	T10665 hypothetical prote
35	71.5	7.4	105	2	T10350 hypothetical prote
36	71.5	7.4	627	2	B71709 conserved hypothet
37	71	7.4	227	2	F72334 probable cell divi
38	71	7.4	414	2	G71331 ABC transporters (
39	71	7.4	473	2	Af1207 protein F4H10.1
40	71	7.4	480	2	G88690 hypothetical prote
41	71	7.4	500	2	T10543 spike glycoprotein
42	71	7.4	660	2	T02768 hypothetical prote
43	70.5	7.3	188	2	H82933 hypothetical prote
44	70.5	7.3	412	2	T24023 S-locus-specific g
45	70.5	7.3	424	2	T14525

ALIGNMENTS

RESULT 1

S43486

B-cell maturation factor - human
N:Alternate names: BCM protein; BCMA protein; BEL protein
C:Species: Homo sapiens (man)
C:Date: 27-Jan-1995 #sequence_revision 27-Jan-1995 #text_change 21-Jul-2000

C:Accession: S43486; S31208; S36661
R:Laabi, Y.; Gras, M.P.; Brouet, J.C.; Berger, R.; Larsen, C.J.; Tsapis, A.
Nucleic Acids Res. 22, 1147-1154, 1994

A:Title: The BCMA gene, preferentially expressed during B lymphoid maturation, is bl

A:Reference number: S43486; MUID:94218235; PMID:8165126

A:Accession: S43486
A:Status: preliminary
A:Molecule type: DNA

A:Residues: 1-184 <LA>

A:Cross-references: EMBL:229574; NID:9471244; PTDN:CAA82690.1; PID:9471245

R:Laabi, Y.; Gras, M.P.; Carbonnel, F.; Brouet, J.C.; Berger, R.; Larsen, C.J.; Tsap

EMBO J. 11, 3897-3904, 1992
A:Title: A new gene, BCM, on chromosome 16 is fused to the interleukin 2 gene by a t

A:Reference number: S31208; MUID:93010984; PMID:1396583

A:Accession: S31208
A:Molecule type: mRNA

A:Residues: 1-184 <LA>
A:Cross-references: EMBL:214954; NID:929407; PTDN:CAA78679.1; PID:929408

A:Status: preliminary
A:Molecule type: mRNA

A:Residues: 4-164 <LA>
A:Cross-references: EMBL:214955

C:Genetics:
A:Gene: GDB:BCMA

A:Cross-references: GDB:135977; OMIM:109545
A:Map position: 16p13.1-16p13.1

A:Insertions: 44/1; 93/1
C:Superfamily: human B-cell maturation factor

Query Match

Best Local Similarity 100.0%; Pred. No. 5.6e-81;

Matches 184; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY	1	MLOMAGCCSONEYFDSLHACIPCOLRCSSNTPPLTCORVCNASTVTSVGTNAIIMTCL	60
DB	1	MLOMAGCCSONEYFDSLHACIPCOLRCSSNTPPLTCORVCNASTVTSVGTNAIIMTCL	60
OY	61	GLSLIISLAVFVLMFLRKISSEPLKDEFKFTGSGLLGMANIDLEKSRITDEIILPRGLE	120
DB	61	GLSLIISLAVFVLMFLRKISSEPLKDEFKFTGSGLLGMANIDLEKSRITDEIILPRGLE	120
OY	121	YVTEECTCEDCIKSRKPVSDHCPLPAMEGATILVYTKINDCKSLPALSAATEIKS	180
DB	121	YVTEECTCEDCIKSRKPVSDHCPLPAMEGATILVYTKINDCKSLPALSAATEIKS	180

Qy	181	ISAR	184
Db	181	ISAR	184

RESULT 2
C97344
amino acid ABC transporter, permease component CAC3519 [imported] - Clostridium acetobutylicum

R. Nolling, J.; Bretton, G.; Omechecheko, M. V.; Markarova, K. S.; Zeng, Q.; Gibson, R.; Lee, D.; Daly, M. J.; Bennett, G. N.; Koonin, E. V.; Smith, D. R. *Phys. Rev. Lett.* **102**, 102202 (2009).

A;Accession: C9273AA
A;Reference number: A96900; MWID:21359325; PMID:21359325

A:Residue: 1-217 <RIB>
A:Molecule type: DNA
A:status: preliminary

A; Cross-references: GB:AE001437; PIDN:AAK8152.1; PID:q15026719; GSPDB:CN001668
A; Experimental source: Clostridium acetobutylicum ATCC824

A;Gene: CAC3619
C;Superfamily: histidine permease protein M

Query Match	9.28;	Score 88.5;	DB 2;	Length 217;
Best Local Similarity	24.88;	Pred. No. 0.98;		
Matches 55;	Conservative 25;	Mismatches 77;	Indels 65;	Gaps 10

QY 16 SLHACIPCCQRCSSNPPLTCQRYCNASV-----TNSVKGTNAI----LWYCLGL 62

DQ 4 SLNKNVIPVLLDGTRIALLTCSIIIGCIIGTIAMKFTSSVKVLNLGKFYTWILRG 63

```

Qy 63 SLISLAVFV--LMLFLRKISSEPLKDFE-----KNTGS-----GLLGMANIDLEKSR 109
      ::::: ::::: ::::: ::::: ::::: ::::: ::::: ::::: ::::: :::::
Db 64 PLLIQLYVYVYGLPFLSDKLTNTVPMKAAIIGLSNLSGAVTAEIRGCIALIDNGQFEASK 122

```

```

QY 109 -----TGDEILRLRGLEYIVEEC-----TCEDCI-KSKPKVDSBH 142
      |  ||| : : | | : : | |
Db 124 ALGLTYGQTKRKRIILPQAIRVIVPPCGNEFIAMIKDTSLSVITMELLRKQLLVSSG 183

```

```

QY      143 CFP LPAMEGA--TIVTTRKNDYCKSLPALSA TEI EK SIS 182
          | : | | | : |
Db      184 DAVTPYLFAGIFYLITTTIETGIFSK-----IEKKLS 215

```

RESULT
T088881

C:Species: Mus musculus (house mouse)
C:Date: 11-Jun-1999 #sequence_revision 11-Jun-1999 #text_change 21-Jul-2000

C/Accession: 100001
R/Welgmann, A.; Corbell, D.; Hellwig, A.; Huttner, W.B
Proc Natl Acad Sci U S A 94 12425-12430 1997

A:Title: Promilin, a novel microvilli-specific polytopic membrane protein of the apical
A:Reference number: Z16512; MUID:98024147; PMID:9356465

A;Accession: T08881
A;Status: preliminary; translated from GB/EMBL/DBJ

A;Residues: 1-858 <ME1>
n;Molecule type: minin
Cross-references: FMB1:AF026269. NTD:G2559003. PIDN:AA86715.1. PID:G2559006

A:Experimental source: kidney
C:keywords: glycoprotein; membrane protein

Query Match	9.08;	Score 86.5;	DB 2;	Length 858;
Best Local Similarity	22.78;	Pred. No. 6;		
Matches 44;	Conservative 30;	Mismatches 67;	Indels 53;	Gaps 10

OY 18 LKACIPCOLRCSSNPPPLTCORRYCMASVTSNVGTNAIMLTCLGSLIISLAVFLMRLL 77
| | | | : | : | : | : | : |
DB 117 LVGCFCFCMKC-----CNK-CGGEHQROKONAPCRKCKGLSLLVICILMSGLIIY 167

```

0Y 78 RKSSPEPKDEFKNTGSGLLGMANIDEXSRIGD-ELIY--PGLLEYVECTCE---- 129
    ::: : | | | | : : | : : : | | : |
Db 168 GFVANOQTFRIRIKIGOK-----LAKSNFEDFOTILLETPKRIDYVEQYTNFNKKA 218

```

```

Oy 130 ----DCIKS-----KRVDSHCHFPPLAMEGATILVTTK-TNDYCKSLPAL.- 172
      | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 219 FSDLDIGISVLGGRITQDLKPKV-----TPVLEIKAMATAIKOTKDALQNMSSLSKS 271

```

```

OY      173  --SATEIEKSISA 183
          ::||:: ::|:
Db      272  LQDATAQLNTNLSS 285

```

RESULT 4
T13009
hypothetical protein T24C20.80 - Arabidopsis thaliana

```
C:Date: 13-Aug-1999 #sequence_revision 13-Aug-1999 #text_change 24-Nov-1999
C:Accession: T11006
```

R;Choisine, N.; Robert, C.
submitted to the Protein
A;Reference number: 217586

A:Accession: F13009
A:Molecule type: DNA
A:Residues: 1-1998 <CHOS

A: Cross-references: EMBL:AL096856; GSPDB:GN00061; ATSP:T24C20.80
A: Experimental source: cultivar Columbia; BAC clone T24C20

A:Map position: 3

A: Introns: 71/3; 117/1; 162/3; 230/1; 309/3; 348/2; 396/1; 452/3; 532/2; 604/1; 1005;
C: Superfamily: Arabidopsis thaliana hypothetical protein T24C20.80

Query Match	8.7%;	Score 83.5;	DB 2;	Length 1998;
Best Local Similarity	29.4%;	Pred. No. 27;		
Matches	37;	Conservative	18;	Mismatches 28;
				Indels 43;
				Gaps 9

```

QY      38  QRCNASTNSVKCTNALMTCTGLSLIISLAVFVLMFLKRISSEPLKD-EKKN-~TGS 94
      :||:|  ||  ||  ::  |  |  :  |  ||  |  |
Db      1089  ERYCSA-----NSALGTPSM---C-----SSTGPFQDSEFENFSLGP 1122

```

Qy 95 GUGMANIDLEKSTGDETIILPRGLETVVECTCEDCIKSR-----KVDSHCFFPEAM 149
|:::| | | |:::| | | |
Db 1123 SLVKLSLDM-SRLGD----RGHFFDEGGSCNGRSSAPGLNTGNVNIIDMGDL--M 1173

QY	150	EKGATI	155
	:		
Db	1174	DGKATI	1179

RESULT 5
A57434

N:Alternate names: cell adhesion kinase-beta
C:Species: Rattus norvegicus (Norway rat)

```
C:Date: 08-Feb-1996 #sequence_revision 08-Feb-1996 #text_change 04-Feb-2
C:Accession: A57434
```

J. Biol. Chem. 270, 21206-21219, 1995

A;Accession: A57434

A;Molecule type: mRNA
A;Residues: 1-1009 <5'

C: Superfamily: unassigned Ser/Thr or Tyr-specific protein kinases; protein kinase homology domain
A: Cross-references: GB:D43854; NID:g10006/9; PIDN:BAA038290.1; PID:d10088885; PID:g10006/9; KMD:phosphotransferase, transmembrane, tyrosine-specific protein kinase

F:423-686/Domain: protein kinase homology <KIN>
F:431-439/Region: protein kinase ATP-binding motif

Query Match	8.5%;	Score 82;	DB 2;	Length 1009
Best Local Similarity	26.9%;	Pred. No. 18;		

	Matches	29:	Conservative	13:	Mismatches	34:	Indels	32:	Gaps	4:
QY	88	EKKNTSGGLGMNIDLEKSR-----	-TDELLIRGLEIYEVECTCEDCIKSPPK	138	:			:	:	:
Db	249	KFFET---LGFANIDQERYRCCELLGGMNIYDVLITGRIGRLTSQTPTCLAEFKQL	305	:	:			:	:	:
OY	139	DSDHCFPLPME-----EGATILVTTKTND-----	-YCK	166	:	:		:	:	:
Db	306	RSTICLPLETQAIVLDLGIEGAPOSISTISTSSLAENMADLIDGYLR	353	:	:		:	:	:	:

RESULT 6

C:Species: Paramesicium tetraurelia
 C:Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 07-Dec-1999
 C:Accession: T28669
 R:Nielsen, E., You, Y., Forney, J.
 J. Mol. Biol. 222, 835-841, 1991
 A:Title: Cysteine residue periodicity is a conserved structural feature of variable surf
 A:Reference number: Z20504; MUID:92106337; PMID:1762150
 A:Accession: T28669
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: DNA
 A:Residues: 1-223 <NIE>
 A:Cross-references: EMBL:M65164; NID:g15974; PID:g15975; PIDN:AAA61740.1
 C:Genetics:
 A:Genetic code: SGC5

Query Match	8.5%;	Score 81.5;	DB 2;	Length 2233;
Best Local Similarity	25.1%;	Pred. NO. 45;		
Matches 43;	Conservative 17;	Mismatches 58;	Indels 53;	Gaps 10

```

Oy      6 GQCSQNEFFDLSLHACIPQQLKRCSSNPPETLCQRXCA-SVTNSYKGTNALILWTCLGISL 64
      | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db      520 GSCYKQ-----CSASQDNTHTAQCCEYLPACTLSNTKKG-----CIDPL 561

```

```
Oy      65  TISLAVFLVLMFLRKISSEPLDEEFKNTGSLGMANIDL----EKSRTGEIILPRGLE 1200
           | : : : | : : : | : : : | : : : | : : : | : : : | : : : |
Db    562 TCSA-----LVKENCGLKANREK---CGWTSSTCVDIIVCTTAPTKTDD-----D 6030
```

```

Oy      121 YTVEECTC---EDCIKSPKVDSDHCFPPAMEEGATI----LVTTKTN 162
      ||| | :| | | | | | | | | | | | | | | | | | | | | |
Db      604 YTVELCEAYKPPSNCV---PNGTKKGCMELAKCESRTIKEOCDDVAGTKTN 651

```

RESULT

protein R08P11.7 [imported] - Caenorhabditis elegans
C:Species: Caenorhabditis elegans
C:date: 10-May-2001 #sequence_revision 10-May-2001 #text_change 17-May-2002
C:Accession: D89010
R:nonymous, The C. elegans Sequencing Consortium.
Science 282, 2012-2018, 1998
A:title: Genome sequence of the nematode C. elegans: a platform for investigating biology
A:Note: see webstites genome.wustl.edu/gsc/C.elegans/ and www.sanger.ac.uk/Projects/C.elegans/
A:Note: published errata appeared in Science 283, 35, 1999; Science 283, 2103, 1999; and
A:Accession: D89010
A:status: preliminary
A:Molecule type: DNA
A:Residues: 1-773 <STO>
A:Cross-references: GBCHR.V: PIDN:AAB54249.1; PID:g2088832; GSPDB:GN0023; CESP:R08P11
A:Note: Similar to peroxidase
C:genetics:
A:Gene: R08P11.7
A:map position: 5
C:Superfamily: myeloperoxidase; myeloperoxidase homology

Query Match 8.4%; Score 81; DB 2; Length 773;
Best Local Similarity 21.7%; Pred. No. 17;
Matches 40; Conservative 25; Mismatches 91; Indels 28; Gaps 6.

[illegible]

RESULT 8

N:Alternative names: cell adhesion kinase-beta
C:Species: Homo sapiens (man)
C:Date: 10-Apr-1996 #sequence, revision 27-Feb-1997 #text_change 17-Nov-2000
A:Accession: S60248: 602330: B57434
R:iley, S., Moreno, H., Martinez, R., Canoll, P., Peles, E., Musacchio, J.M., Plozman
N:ature 376, 737-745, 1995
A:Title: Protein tyrosine kinase PYK2 involved in Ca(2+)-induced regulation of ion ch
A:Reference number: S60248: M01D:95179967: PMID:754443
A:Accession: S60248
A:Status: preliminary; nucleic acid sequence not shown

A./Cross-references: EMBL:U33284; NID:g988304; PIDN:AMC50203.1; PID:g988305
R/Sasaki, T.; Nagura, K.; Sasaki, H.
submitted to the EMBL Data Library, December 1995

A/Accession: G02330
A/Status: preliminary; translated from GB/EMBL/DBJ
A/Molecule type: mRNA

A: Cross-references: EMBL:U043522; NID:g1165218; PION:MAC05330.1; PID:g1165219
R:Sasaki, H.; Nagura, K.; Ishino, M.; Tobioke, H.; Kotani, K.; Sasaki, T.
J. Biol. Chem. 270, 21206-21219, 1995

A:Reference number: A57434; MUID:95403356; PMID:
A:Accession: B57434
A:Status: preliminary

A;Residues: 1-22, 'G', 24-150 <SA2>
A;Cross-references: GB:D45853; NI
C;Genetics:

C:Superfamily unassigned Ser/Thr or Tyr-specific protein kinases; protein kinase h
C:Keywords: ATP; phosphotransferase; tyrosine-specific protein kinase
F:423-686/pdomain: protein kinase homology <KIN>
F:431-439/Region: protein kinase ATP-binding motif

Query Match	8.2%;	Score 79.5;	DB 2;	Length 1009;
Best Local Similarity	32.1%;	Pred. No. 31;		
Matches 25; Conservative	9;	Mismatches 29;	Indels 15;	Gaps 3;

```

02  EFKNITSGLLGMANIDERSK-----TGDLEILPRGIEIVECTCEDIKSRKV 138
      ::||  |  |  |||  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
Db  249  KFEFT---LACFANIDQETRYCELIQGMNITVDLVIGPKGIROLTSODAKPICLAERKQI 305

```

```

QY      139  DSDHCFPLPAMEEGATIL 138
          |  |  |  |  |  |  |
Db      306  RSIRCLPL--EEGQAVL 320

```

RESULT

T43251
furin (EC 3.4.21.75) - fall armyworm

N:Alternate names: paired basic amino acid cleaving enzyme; proprotein convertase; serin
 C:Species: Spodoptera frugiperda (fall armyworm)
 C>Date: 11-Jan-2000 #sequence_revision 11-Jan-2000 #text_change 11-Jan-2000
 C:Accession: T43251
 R:Cieplik, M.; Klenk, H.
 Submitted to the EMBL Data Library, January 1996
 A:Description: Cloning and functional characterization of FURIN from Spodoptera frugiper
 A:Reference number: 223368
 A:Accession: T43251
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: mRNA
 A:Residues: 1-1299 <CIE>
 A:Cross-references: EMBL:Z68888; NID:G157859; PID:e219690; PIDN:CA93116.1
 A:Experimental source: Clone Sturin 6; ovary
 A:Function:
 A:Description: responsible for the endoproteolytic processing of proproteins with specif
 C:Keywords: hydrolase; serine proteinase

Query Match 8.1%; Score 79.5; DB 2; Length 1299;
 Best Local Similarity 24.1%; Pred. No. 40;
 Matches 39; Conservative 26; Mismatches 48; Indels 49; Gaps 11;

OY 8 CSQNEFDSLHACIPCOLRCS-----SNRPPLTCORYNAS-----VTNSVKTNAIL-W 57
 DB 1150 CSRLPLIDRLNMQVCPC---CSEKGVNTSTPTDC-CHCNPMENECINSVAGKRRIAEW 1205
 OY 58 TCGLS-----LITSLAV-----FVLMFLRKISSEPLKDEFKNTSGLLGMAN 101
 DB 1206 GALTTPASDAAPSAVAVTIANCAAVGLFTVLVAVDANSHPREKTRKTSVNG----- 1259
 OY 102 IDEKSRGTDEIILPR-CLEVTVECTCEDCISKRPVDSOH 142
 DB 1260 -VEYSR-----LPRTDVDFTV-----LTCTDQEGPEYEH 1289

RESULT 10
 D64469
 POTASSIUM channel homolog - Methanococcus jannaschii
 C:Species: Methanococcus jannaschii
 C>Date: 13-Sep-1996 #sequence_revision 13-Sep-1996 #text_change 21-Jul-2000
 C:Accession: D64469
 R:Bull, C.J.; White, O.; Olsen, G.J.; Zhou, L.; Fleischmann, R.D.; Sutton, G.G.; Blake,
 / Reich, C.J.; Overbeek, R.; Kirkness, E.F.; Weinstock, K.G.; Merrick, J.M.; Glodek, A.;
 rson, J.D.; Sadow, P.W.; Hanna, M.C.; Cotton, M.D.; Roberts, K.M.; Hurst, M.A.
 Science 273, 1058-1073, 1996
 A:Authors: Kaine, B.P.; Borodovsky, M.; Klenk, H.P.; Fraser, C.M.; Smith, H.O.; Woese, C
 A:Title: Complete genome sequence of the methanogenic archaeon, Methanococcus jannaschii
 A:Reference number: A64300; MUID:96337999; PMID:8688087
 A:Accession: D64469
 A:Status: preliminary; nucleic acid sequence not shown; translation not shown
 A:Molecule type: DNA
 A:Residues: 1-343 <BOL>
 A:Cross-references: GB:U67575; GB:U77117; NID:G1591992; PIDN:AB99365.1; PID:G1592000; T
 C:Genetics:
 A:Map position: REV1308326-1307295
 C:Superfamily: conserved hypothetical protein s110993

Query Match 8.1%; Score 78.5; DB 2; Length 343;
 Best Local Similarity 20.4%; Pred. No. 13;
 Matches 39; Conservative 35; Mismatches 66; Indels 51; Gaps 8;

OY 12 EYDSSLHACIPCOLRCSNRPPLTCORYNASVTNSVKTNAILMTCTGLSLITSLAVF 71
 DB 32 DFTALYFSVLT-----TITTCYGDPRKPTFLGRITLVVAVCGVGIWYLFSL 80
 OY 72 VLMFL-----LRKISS--EPLKDEFKNTSGLLGMA-----NIDLEKSRGTD 111
 DB 81 IAFEIVGEKFEFVRLLKMKNNIKTLKHVYICGYRLGKVGVEKFEIEHPIPLAIDINE 140
 OY 112 EII-----LPGLEIVYEECTCEDCISKRPV-----DSDKCF-PLPAMEGC 152
 DB 141 DVLTKEEYKPPKFLYIVGDAAKKEVVK-KAKIDKAGLIATLPSSADNVFLTLARLEIN 199

OY 153 ATILVTTKTND 163
 DB 200 PNILITAKADE 210

RESULT 11
 JC5894
 Killer cell inhibitory receptor p91A precursor - mouse
 C:Species: Mus musculus (house mouse)
 C>Date: 18-Mar-1998 #sequence_revision 18-Mar-1998 #text_change 17-Mar-1999
 C:Accession: JC5894
 R:Imashinita, Y.; Fukuta, D.; Tsuji, A.; Nagabukuro, A.; Matsuda, Y.; Nishikawa, Y.; O
 J. Biochem. 123, 358-368, 1998
 A:Title: Genomic structures and chromosomal location of p91, a novel murine regulator
 A:Reference number: JC5894; MUID:98218758; PMID:9538215
 A:Accession: JC5894
 A:Status: nucleic acid sequence not shown
 A:Molecule type: DNA
 A:Residues: 1-841 <YAM>
 A:Cross-references: GB:AF040946
 C:Comment: This protein function as inhibitory cell-surface molecule against cell act
 C:Genetics:
 A:Map position: 7
 F:1-24/Domain: signal sequence #status predicted <SIG>
 F:24-841/Product: killer cell inhibitory receptor p91A #status predicted <MAT>
 F:24-118, 119-220, 221-315, 316-418, 419-517, 518-618/Domain: extracellular Ig-like #statu
 F:616-674/Domain: transmembrane #status predicted <TM>
 F:675-765/Domain: cytoplasmic #status predicted <CT>

Query Match 8.1%; Score 78; DB 2; Length 841;
 Best Local Similarity 22.7%; Pred. No. 35;
 Matches 46; Conservative 32; Mismatches 61; Indels 64; Gaps 9;

OY 9 SONEFDSLHACIPCOLRCS-----SNRPPLTCORYNASVTNSVKTNAILMTCTGLSL 64
 DB 598 AONSSFYLLSSASAPVELVAVSCPIETSTPPT-----MSMPLGLMHTYALALIGVSV 649
 OY 65 TISLAVVLMFL--RKISSEPLKDEFKNTSGLLGMANIDLKSRGTDEIILPRG---- 118
 DB 650 AFLTFLPILFIFILRLRRHGRKPKDQKEX-----DLQSSGAEPIYRKGELOK 699
 OY 119 -----LEVTVECTCEDCIR-----SKRPVDSHDCPLPAMESEATVLTNTKN 162
 DB 700 RRPAPAAOTEESIXASVEDMQEDVCEVLSMTTPRED-----PQGT----- 741
 OY 163 DYCKSLPAL-SATELEKSISAR 184
 DB 742 -YAOVKPSRLRKRAKGVSPSVSR 763

RESULT 12
 D86345
 hypothetical protein F16F4.10 [imported] - Arabidopsis thaliana
 C:Species: Arabidopsis thaliana (mouse-ear cress)
 C>Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 17-May-2002
 C:Accession: D86345
 R:Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alon
 anson, N.F.; Hughes, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar,
 Nature 408, 816-820, 2000
 A:Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim,
 C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maiti, R.; Marzla
 Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.
 A:Authors: Salzberg, S.L.; Schwartz, J.R.; Shim, P.; Southwick, A.M.; Sun, H.; Tallo
 ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.
 A:Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.
 A:Reference number: AB6141; MUID:21016719; PMID:11130712
 A:Accession: D86345
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-738 <STO>
 A:Cross-references: GB:AB005172; NID:98920639; PIDN:AAF81361.1; GSPDB:GN00141
 C:Genetics:

A:Map position: 1
C:Superfamily: Arabidopsis probable serine/threonine-specific protein kinase PRO25; prot

Query Match 8.0%; Score 77.5; DB 2; Length 738;
Best Local Similarity 26.2%; Pred. No. 34;
Matches 28; Conservative 21; Mismatches 45; Indels 13; Gaps 5;

OY 8 GSONEYPSLL-HACIPOLCSSLTPPLTCORCMASVNSYKGNALIMTCLGLSLTI 66
DB 294 CGSDSTCEKRLCHFRNCRCRRELTNTNCKPKRNEY--VEMTIVLGTIGF-LVI 349
OY 67 SLAVFLMFLRKISSEPLKDE-FKNTGSGLL-----GMANIDLE 105
DB 350 LTAISCIEHKMKNTKDTLROQFQNGGGMRLSGAGPSNVDAK 396

RESULT 13

T01733
Hypothetical protein A_IC002N01.31 - Arabidopsis thaliana

C:Species: Arabidopsis thaliana (mouse-ear cress)

C>Date: 19-Feb-1999 #sequence_revision 19-Feb-1999 #text_change 24-Mar-1999

C:Accession: T01733

R:Scheet, P.; Maggi, L.

submitted to the EMBL Data Library, June 1997

A:Description: The sequence of A. thaliana IC002N01.

A:Reference number: Z14407

A:Accession: T01733

A:Status: translated from GB/EMBL/DBJ

A:Molecule type: DNA

A:Residues: 1-968 <SCH>

A:Cross-references: EMBL:AF007269; NID:g2191126; PID:g2191152

A:Experimental source: cultivar Columbia

C:Genetics:

A:Map position: 4

A:Introns: 112/3; 136/2; 164/3; 237/3; 356/1; 430/1; 460/2; 718/2; 752/3; 781/3; 806/3;

A:Note: A_IC002N01.31

Query Match 8.0%; Score 77.5; DB 2; Length 968;
Best Local Similarity 21.6%; Pred. No. 45;
Matches 35; Conservative 26; Mismatches 62; Indels 39; Gaps 5;

OY 43 ASYTSVSKC---TNAITMTCGLSLIISLAVPYLM-----FLRKISSEPLK 86
DB 770 SSITDSISGVGESSDGVSAAGLSVFAPTEDRKQTLKQVDEFPLTKVAPKELY 829
OY 87 DEFKMGSGLLGMANIDLEKSRGTDEIILPRGLETVVEECTCEDCKSRKVDSDHCFPL 146
DB 830 DELKEIGKAL-----LPQSTSNKALPAPATVTAESAATATTIVDKP----- 872
OY 147 PMNEGATILVTKTND---YCKSLPALSAETIEKSISAR 184
DB 873 --VPEETVAATTTVDKPVEPEVPEVPAIEAANAQ 912

RESULT 14

T45824

hypothetical protein F2K15.50 - Arabidopsis thaliana

C:Species: Arabidopsis thaliana (mouse-ear cress)

C>Date: 04-Feb-2000 #sequence_revision 04-Feb-2000 #text_change 20-Jun-2000

C:Accession: T45824

R:Rieger, M.; Gabel, C.; Mueller-Auer, S.; Schaefer, M.; Zipp, M.; Mewes, H.W.; Lemcke, submitted to the Protein Sequence Database, January 2000

A:Reference number: 223015

A:Accession: T45824

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-522 <RIE>

A:Cross-references: EMBL:AL132956

A:Experimental source: cultivar Columbia; BAC clone F2K15

C:Genetics:

A:Map position: 3

A:Introns: 69/3; 271/3; 294/1; 327/3; 397/3; 443/3

A:Note: F2K15.50

C:Superfamily: Arabidopsis thaliana hypothetical protein F2K15.70

Query Match 8.0%; Score 77; DB 2; Length 522;
Best Local Similarity 27.0%; Pred. No. 27;
Matches 27; Conservative 18; Mismatches 37; Indels 18; Gaps 3;

OY 16 SLIHAC-----IPCOLCSSLTPPLTCORCMASVNSYKGNALIMTC--IG 61
DB 159 SLVLCMKRTSNPDELPSLPYQYKSSRSLSLTIGSSDSRLMLVK---VIMTVAILG 214
OY 62 LSLISLAVFLMFLRKISSEPLKDEFKNTGSGLLGMAN 101
DB 215 LNTVCDALEFIYTLFLVKDTERPIKGDPLSKRSQRLVH 254

RESULT 15

F72288
methyl-accepting chemotaxis protein - Thermotoga maritima (strain MSB8)

C:Species: Thermotoga maritima

C>Date: 11-Jun-1999 #sequence_revision 11-Jun-1999 #text_change 21-Jul-2000

C:Accession: F72288

R:Nelson, K.E.; Clayton, R.A.; Gill, S.R.; Gwin, M.L.; Dodson, R.J.; Haft, D.H.; Hl Garrett, M.M.; Stewart, A.M.; Cotton, M.D.; Pratl, M.S.; Phillips, C.A.; Richardson, C.M.

Nature 399, 323-329, 1999

A:Title: Evidence for lateral gene transfer between Archaea and Bacteria from genome

A:Reference number: A72200; MUID:99287316; PMID:10360571

A:Accession: F72288

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-539 <ARR>

A:Cross-references: GB:AE001772; GB:AE000512; NID:g4981693; PIDN:AA036222.1; PID:g498

A:Experimental source: strain MSB8

C:Genetics:

A:Gene: TM1146

C:Superfamily: methyl-accepting chemotaxis protein

Query Match 8.0%; Score 77; DB 2; Length 539;
Best Local Similarity 32.0%; Pred. No. 28;
Matches 24; Conservative 19; Mismatches 20; Indels 12; Gaps 5;
OY 42 NASVTSVKGNTAIIIMTCGLSLIISLAVPYLMFLRKISSEPLKD---EFKNTGSGLLG 98
DB 150 NWSMTKNIK-RNIIFF---LVVCAAMFAIFTTNTLT-PLKLAIVAVENLSHGLV- 202
OY 99 MANIDLEKSRGTDEI 113
DB 203 --NVEIEKIRSKDEI 215

Search completed: November 12, 2002, 17:01:01
Job time : 31.4292 secs

GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on: November 12, 2002, 16:49:26 ; Search time 15.794 Seconds
(without alignments)
483.199 Million cell updates/sec

Title: US-09-848-271-2
Perfect score: 964
Sequence: 1 M0MAGQCSQNEYPDSLHA.....CKSLPALSAETEIEKISAR 184

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 112892 segs, 41476328 residues

Total number of hits satisfying chosen parameters: 112892

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database: SwissProt_40:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	964	100.0	184	TR17_HUMAN	Q02223 homo sapien
2	572	59.3	185	TR17_MOUSE	Q08472 mus musculu
3	116.5	12.1	175	T13C_MOUSE	Q9D8D0 mus musculu
4	94	9.8	323	TNR6_BOVIN	P51867 bos taurus
5	93	9.6	184	T13C_HUMAN	Q96133 homo sapien
6	86.5	9.0	867	PROM_MOUSE	Q54990 mus musculu
7	82	8.5	1009	FAK2_MOUSE	Q9QVP9 m. protein t
8	82	8.5	1009	FAK2_RAT	P70600 rattus norv
9	79.5	8.2	1009	FAK2_HUMAN	Q14289 h. protein t
10	78.5	8.1	293	T13X_HUMAN	Q14826 homo sapien
11	78.5	8.1	343	YD57_METU	Q58752 methanococ
12	77	8.0	249	T13X_MOUSE	Q96135 mus musculu
13	75.5	7.8	638	YCSB_SCHPO	Q74910 schizosacch
14	75	7.8	849	SRK6_BRAOL	Q09092 brassica ol
15	74.5	7.7	384	ERL1_KLULA	P41771 kluvercomyc
16	72.5	7.5	1013	PRML_DROME	P82295 drosophila
17	71.5	7.4	105	Y078_NPYOP	Q10331 corylia pseu
18	71.5	7.4	627	Y017_RICR	Q3266 ticketasia
19	71	7.4	227	COMB_THENA	Q3266 thermotoga
20	70.5	7.3	188	Y101_UREPA	Q3P143 ureaplasma
21	70.5	7.3	1203	MGR5_RAT	P31424 rattus norv
22	70.5	7.3	1877	PCRS_MOUSE	Q04592 mus musculu
23	70.5	7.3	2715	G156_PAPR	P13387 paramedico
24	70	7.3	654	HS70_TRIRU	Q93866 trichophyto
25	69.5	7.2	573	TUPC_BACSU	P41594 bacillus su
26	69.5	7.2	1212	MGR5_HUMAN	P41594 homo sapien
27	69.5	7.2	5376	ZAN_MOUSE	Q08789 mus musculu
28	69	7.2	324	GCI_MOUSE	P01868 mus musculu
29	69	7.2	352	CSAR_RAT	P97520 rattus norv
30	69	7.2	379	PANE_YEAST	P18787 saccharomyc
31	69	7.2	393	GCJM_MOUSE	P01869 mus musculu
32	69	7.2	416	R23B_MOUSE	P47278 mus musculu
33	68.5	7.1	321	OSV1_HUMAN	Q9UG66 homo sapien

34	68.5	7.1	328	1	Y679_CHLMO	Q9P127 chlamydia m
35	68.5	7.1	409	1	R33B_HUMAN	P54727 homo sapien
36	68.5	7.1	575	1	CH62_CUCWA	Q05046 cucurbita m
37	68.5	7.1	576	1	CH62_MAIZE	Q43298 zea mays (m
38	68.5	7.1	577	1	CH61_MAIZE	P29185 zea mays (m
39	68	7.1	590	1	ACCD_PEA	P18823 pisum sativ
40	68	7.1	1140	1	RA18_SCHPO	P53692 schizosacch
41	68	7.1	1203	1	XOPE_XENLA	P50533 xenopus lae
42	68	7.1	2158	1	MY9B_HUMAN	Q13439 homo sapien
43	68	7.1	3386	1	POLG_DENA	P09866 d genome po
44	67.5	7.0	178	1	LACB_BOVIN	P02754 bos taurus
45	67.5	7.0	245	1	YH77_ARCFU	Q28497 archaeoglob

ALIGNMENTS

RESULT 1	ID	TR17_HUMAN	STANDARD:	PRT:	184 AA.
AC	Q02223;				
DT	01-JUL-1993	(Rel. 26, Created)			
DT	01-JUL-1993	(Rel. 26, Last sequence update)			
DT	15-JUN-2002	(Rel. 41, Last annotation update)			
DE	Tumor necrosis factor receptor superfamily member 17 (B-cell maturation protein).				
GN	TNFRSF17 OR BCM4 OR BCM.				
OS	Homo sapiens (Human).				
CC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.				
OX	NCBI_TaxID=9606;				
LN	[1]				
RP	SEQUENCE FROM N.A., AND CHROMOSOMAL TRANSLOCATION.				
RC	TISSUE-Peripheral blood leukocytes, and Lymph node;				
RX	MEDLINE=93010984; PubMed=1396583;				
RA	Laabi Y., Gras M.P., Carbonnel F., Brouet J.C., Berger R., Larsen C.J., Tsapis A.;				
RT	"A new gene, BCM, on chromosome 16 is fused to the interleukin 2 gene by a t(4;16)(q26;p13) translocation in a malignant T cell lymphoma.";				
RL	EMBO J. 11:3897-3904(1992).				
LN	[2]				
RP	SEQUENCE FROM N.A.				
RX	MEDLINE=94218235; PubMed=8165126;				
RA	Laabi Y., Gras M.P., Brouet J.C., Berger R., Larsen C.J., Tsapis A.;				
RT	"The BCM gene, preferentially expressed during B lymphoid maturation, is bidirectionally transcribed.";				
RL	Nucleic Acids Res. 22:1147-1154(1994).				
LN	[3]				
RP	SEQUENCE FROM N.A.				
RX	MEDLINE=99425270; PubMed=10493829;				
RA	Loftus B.J., Kim U.-J., Shedd V.P., Kalush F., Brandon R., Fuhrmann J., Mason T., Crosby M.L., Barnstead M., Cronin L., Deslattes Mays A., Cao Y., Xu R.X., Kang H.-L., Mitchell S., Elchler E.E., Harris P.C., Venter J.C., Adams M.D.;				
RT	"Genome duplications and other features in 12 Mb of DNA sequence from human chromosome 16p and 16q.";				
RL	Genomics 60:295-308(1999).				
LN	[4]				
RP	SEQUENCE FROM N.A., AND VARIANT THR-153.				
RX	MEDLINE=21419161; PubMed=11528522;				
RA	Kawasaka A., Tsuchiya N., Fukazawa T., Hashimoto H., Tokunaga K.;				
RT	"Presence of four major haplotypes in human BCM4 gene: lack of association with systemic lupus erythematosus and rheumatoid arthritis.";				
RL	Genes Immun. 2:276-279(2001).				
LN	[5]				
RP	FUNCTION.				
RX	MEDLINE=20363816; PubMed=10903733;				
RA	Hatzoglou A., Rousset J., Bourgade M.-F., Rogier E., Madry C., Inoue J., Devigne O., Tsapis A.;				
RT	"TNF receptor family member BCM4 (B cell maturation) associates with TNF receptor-associated factor (TRAF) 1, TRAF2, and TRAF3 and activates NF-kappa B, elk-1, c-Jun N-terminal kinase, and p38				

RT mitogen-activated protein kinase.*;
 RL [6] Immunol. 165:1322-1330(2000).
 RP FUNCTION.
 RX MEDLINE=20259066; PubMed=10801128;
 RA Gross J.A., Johnston J., Mudri S., Enselman R., Dillon S.R.,
 RA Madden K., Xu W., Parrish-Novak J., Foster D., Lofton-Day C.,
 RA Moore M., Little A., Grossman A., Haugen H., Foley K., Blumberg H.,
 RA Harrison K., Kindsvogel W., Clegg C.H.,
 RT "TRAC1 and BCMA are receptors for a TNF homologue implicated in B-cell
 RT autoimmune disease.*;
 RL Nature 404:995-999(2000).
 RP FUNCTION, AND INTERACTION WITH APRIL AND BAFF.
 RX MEDLINE=21170294; PubMed=10973284;
 RA Yu G., Boone T., Delaney J., Hawkins N., Kelley M., Ramakrishnan M.,
 RA McCabe S., Qiu W.R., Kornuc M., Xia X.-Z., Guo J., Stolina M.,
 RA Boyle W.J., Sarosi I., Hsu H., Senaldi G., Thellin L.E.,
 RT "APRIL and TALL-1 and receptors BCMA and TRAC1: system for regulating
 RT humoral immunity.*;
 RL Natl. Immunol. 1:252-256(2000).
 RP INTERACTION WITH TRAF5 AND TRAF6.
 RX MEDLINE=20381353; PubMed=10908663;
 RA Shu H.-B., Johnson H.;
 RT "B cell maturation protein is a receptor for the tumor necrosis factor
 RT family member TALL-1.*;
 RL Proc. Natl. Acad. Sci. U.S.A. 97:9156-9161(2000).
 CC -1- FUNCTION: Receptor for TNFSF13B/BLys/BAFF and TNFSF13/APRIL.
 CC Promotes B-cell survival and plays a role in the regulation of
 CC humoral immunity. Activates NF-kappa-B and JNK.
 CC -1- SUBUNIT: Associates with TRAF1, TRAF2, TRAF3, TRAF5 and TRAF6.
 CC and perinuclear Golgi-like structures.
 CC -1- TISSUE SPECIFICITY: Expressed in mature B-cells, but not in T-
 CC cells or monocytes.
 CC -1- DISEASE: A FORM OF T-CELL ACUTE LYMPHOBLASTIC LEUKEMIA (T-ALL) IS
 CC CHARACTERIZED BY A CHROMOSOMAL TRANSLOCATION T(4;16)(Q26;P13)
 CC WHICH INVOLVES BCMA AND IL2.
 CC -1- SIMILARITY: CONTAINS 1 TNFR-CYS REPEAT.
 CC -----
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 CC -----
 DR EMBL: Z14954; CAA78679.1; -;
 DR EMBL: Z29575; CAA82691.1; -;
 DR EMBL: Z29574; CAA82690.1; -;
 DR EMBL: U95742; AAB67251.1; -;
 DR EMBL: AB052772; BAB60895.1; -;
 DR PIR: S31208; S31208.
 DR PIR: S31209; S31209.
 DR Genew: HGNC:11913; TNFRSF17.
 DR MIM: 109545; -;
 KW Receptor; Immune response; proto-oncogene; signal-anchor;
 KW Transmembrane; Chromosomal translocation; Polymorphism.
 KW DOMAIN 1 34
 FT TRANSSEM 55 77
 FT SIGNAL-ANCHOR (TYPE III MEMBRANE PROTEIN)
 FT (POTENTIAL).
 FT DOMAIN 78 184
 FT REPEAT 7 41
 FT SIZE 3 4
 FT DISULFID 8 21
 FT DISULFID 24 37
 FT DISULFID 28 41
 FT VARIANT 153 153
 FT A -> T.
 FT /FTID=VAR_012234.
 FT SEQUENCE 184 AA; 20138 MW; 277AF11E2767D932 CRC64;

Query Match 100.0%; Score 964; DB 1; Length 184;
 Best Local Similarity 100.0%; Pred. No. 1,3e-83;
 Matches 184; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 OY 1 MLOWAGCQSQNEVYFDSILHACIPQRCSSNTPPTTCQRYCNASVTSNKTNAIWTCL 60
 DB 1 MLOWAGCQSQNEVYFDSILHACIPQRCSSNTPPTTCQRYCNASVTSNKTNAIWTCL 60
 OY 61 GLSLIISLAVYVLMFLFKRISSEPLDKERKNGSGILGNANIDLEKSTGGEIILPGL 120
 DB 61 GLSLIISLAVYVLMFLFKRISSEPLDKERKNGSGILGNANIDLEKSTGGEIILPGL 120
 OY 121 YVEECTCEDCIKSPKVDSDHCFPPAMEEGATILVTPTKNDYCKSLPALASATEIEKS 180
 DB 121 YVEECTCEDCIKSPKVDSDHCFPPAMEEGATILVTPTKNDYCKSLPALASATEIEKS 180
 OY 181 ISAR 184
 DB 181 ISAR 184
 OY 181 ISAR 184
 DB 181 ISAR 184
 RESULT 2
 TR17_MOUSE STANDARD; PRT; 185 AA.
 ID TR17_MOUSE
 AC 088472;
 DT 15-JUN-2002 (Rel. 41, Created)
 DT 15-JUN-2002 (Rel. 41, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Tumor necrosis factor receptor superfamily member 17 (B-cell
 DE maturation protein).
 GN TNFSF17 OR BCMA OR BCM.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI-TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A. (ISOFORMS 1 AND 2).
 RC STRAIN=BALE/C; TISSUE=Spleen;
 RX MEDLINE=99061155; PubMed=9846698;
 RA Madry C., Laabl Y., Callebaut I., Rousset J., Hatzoglou A.,
 RA Le Coniat M., Morron J.P., Berger R., Tsapis A.;
 RT "The characterization of murine BCMA gene defines it as a new member
 RT of the tumor necrosis factor receptor superfamily.*;
 RL Int. Immunol. 10:1693-1702(1998).
 RN [2]
 RP SEQUENCE FROM N.A. (ISOFORM 1).
 RC STRAIN=C57BL/6J; TISSUE=Colon;
 RX MEDLINE=21085660; PubMed=11217851;
 RA Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
 RA Aizawa T., Hara A., Fukunishi Y., Kono H., Adachi J., Fukuda S.,
 RA Aizawa K., Izawa K., Nishi K., Kiyosawa H., Kondo S., Yamada I.,
 RA Saito T., Okazaki Y., Gotohori T., Bono H., Kasukawa T., Saito R.,
 RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
 RA Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,
 RA Kuehl P., Lewis S., Matsuo Y., Nikaide I., Pesole G., Quackenbush J.,
 RA Schmitt L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,
 RA Sakai K., Okido T., Furuno M., Aono H., Balderelli R., Barsh G.,
 RA Blake J., Boffelli D., Bolunga N., Carninci P., de Bonaldo M.F.,
 RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
 RA Gunsberg S., Hill D., Hornann M., Hume D.A., Kamaya K., Lee N.H.,
 RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombereis P.,
 RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
 RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
 RA Suzuki H., Toyooka K., Wang K.H., Weitz C., Whitaker C., Wilming L.,
 RA Wyshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohsaki S.,
 RA Hayashizaki Y.;
 RT "Functional annotation of a full-length mouse cDNA collection.*;
 RL Nature 409:685-690(2001).
 CC -1- FUNCTION: Receptor for TNFSF13B/BLys/BAFF and TNFSF13/APRIL.
 CC Promotes B-cell survival and plays a role in the regulation of
 CC humoral immunity. Activates NF-kappa-B and JNK (by similarity).
 CC -1- SUBUNIT: Associates with TRAF1, TRAF2, TRAF3, TRAF5 and TRAF6 (By

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CC similarity).
CC -1- SUBCELLULAR LOCATION: Type III membrane protein (Probable).
CC -1- ALTERNATIVE PRODUCTS: 2 isoforms; 1 (shown here) and 2; are
CC produced by alternative splicing.
CC -1- TISSUE SPECIFICITY: Detected in spleen, thymus, bone marrow and
CC heart, and at lower levels in kidney and lung.
CC -1- SIMILARITY: CONTAINS 1 TNFR-CYS REPEAT.
CC -----
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CC -----
CC EMBL: AF061505; AAC23799.1; -.
CC EMBL: AK020247; BAB32038.1; -.
CC MGI: MGI:1343050; Tnfrsf17.
CC Receptor; Immune response; signal-anchor; Transmembrane;
CC Alternative splicing.
CC DOMAIN 1 49 EXTRACELLULAR (POTENTIAL).
CC TRANSMEM 50 70 SIGNAL-ANCHOR (TYPE III MEMBRANE PROTEIN)
CC (POTENTIAL).
CC CYTOPLASMIC (POTENTIAL).
CC REPEAT 71 185 TNFR-CYS.
CC DISULFID 5 36 BY SIMILARITY.
CC DISULFID 21 32 BY SIMILARITY.
CC DISULFID 25 36 BY SIMILARITY.
CC VASPLIC 87 91 MISSING (IN ISOFORM 2).
CC SEQUENCE 185 AA; 20442 MW; 8806352BAFD26A8E CRC64;

Query Match 59.38; Score 572; DB 1; Length 185;
Best Local Similarity 62.68; Pred. No. 8.7e-47;
Matches 117; Conservative 21; Mismatches 41; Indels 8; Gaps 4;

OY 4 MAGOCSONEYEDSLHACIPQOLRCSSNTPPLTCQRYCNASVNSYKGNALMTGLGLS 63
DB 1 MAGOCFHEYFDLSLHACKPCHLRCSN--PPATQYCPDPTSSVSKYVLTWFLDT 58
OY 64 LILSLAVFLMLRLKRTSSRLKDEPNK----TGSLLGMANIDLEKSTGTEILLPRLGL 119
DB 59 LVLSLALFTLSFLKRNKPEALDEPDSPEQLDGSQDLKADTELRTRAGDRIEPPSL 118
OY 120 EYTVECTCEDCIRKSPKVDSDHCFPLPAMEGATILVTTKINDYCK-SLPAAL-SATEI 177
DB 119 EYTVECTCEDCIVKSPKGSODHEFPPLPAMEGATILVTTKIGDYGKSSVPTALQSVGM 178
OY 178 EKXSISAR 184
DB 179 EKPIHTR 185

RESULT 3
ID T13C MOUSE STANDARD; PRT; 175 AA.
AC 09BBD0;
DT 15-JUN-2002 (Rel. 41, Created)
DT 15-JUN-2002 (Rel. 41, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Tumor necrosis factor receptor superfamily member 13C (B cell-
DE activating factor receptor) (BAFF receptor) (BAFF-R) (Bly receptor
DE 3) (B-cell maturation defect).
GN TNFRSF13C OR BAFFR OR BCMD OR BR3.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
ON 11
RP SEQUENCE FROM N.A. (ISOFORMS 1 AND 2).
RC STRAIN=BALE/C; TISSUE=B-cell lymphoma;
RX MEDLINE=21442025; PubMed=11509692;
RA Thompson J.S., Bixler S.A., Qian F., Vora K., Scott M.L.,

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RA Cachero T.G., Hession C., Schneider P., Sizing I.D., Mullen C.,
RA Strauch K., Zafari M., Benjamin C.D., Tschopp J., Browning J.L.,
RA Ambrose C.;
RT "BAFF-R, a newly identified TNF receptor that specifically interacts
RT with BAFF."
RL Science 293:2108-2111(2001).
RN [2]
RP SEQUENCE FROM N.A. (ISOFORM 1), AND DISEASE.
RC STRAIN=A/J;
RX MEDLINE=21475520; PubMed=11591325;
RA Yan M., Brady J.R., Chan B., Lee W.P., Hsu B., Harless S.M.,
RA Cancro M.P., Grewal I.S., Dixit V.M.;
RT "Identification of a novel receptor for B lymphocyte stimulator that
RT is mutated in a mouse strain with severe B cell deficiency."
RL Curr. Biol. 11:1547-1552(2001).
RN [3]
RP SEQUENCE FROM N.A. (ISOFORM 1).
RC STRAIN=C57BL/6J; TISSUE=Small intestine;
RX MEDLINE=21085660; PubMed=11217851;
RA Kawal J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
RA Arakawa T., Hara A., Fukunishi Y., Kono H., Adachi J., Fukuda S.,
RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamataka I.,
RA Saito T., Okazaki Y., Gotohori T., Bono H., Kasukawa T., Saito R.,
RA Kaedota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
RA Fleischmann W., Gaasterland T., Gissi C., King B., Kochwa H.,
RA Kuehl P., Lewis S., Matsuo Y., Nikaido I., Resole G., Queckenbush J.,
RA Schiml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,
RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamuya M., Lee N.H.,
RA Lyons P., Marchionni L., Mashima J., Mazarrelli I., Kombergs P.,
RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
RA Suzuki H., Toyooka K., Wang K.H., Weitz C., Whitaker C., Wilming L.,
RA Wyszynski Y., Yoshida K., Hasegawa Y., Kawaji H., Kohlsaki S.,
RA Hayashizaki Y.;
RT "Functional annotation of a full-length mouse cDNA collection."
RL Nature 409:685-690(2001).
RN [4]
RP FUNCTION.
RX MEDLINE=21614654; PubMed=11747827;
RA Harless S.M., Lentz V.M., Sah A.P., Hsu B.L., Clise-Dwyer K.,
RA Hilbert D.M., Hayes C.E., Cancro M.P.;
RT "Competition for BlyS-mediated signaling through Bcmd/BR3 regulates
RT peripheral B lymphocyte numbers."
RL Curr. Biol. 11:1986-1989(2001).
CC -1- FUNCTION: B-cell receptor specific for TNFRSF13B/TNALL/BAFF/BlyS.
CC Promotes the survival of mature B-cells and the B-cell response.
CC -1- SUBCELLULAR LOCATION: Type III membrane protein (Probable).
CC -1- ALTERNATIVE PRODUCTS: 2 isoforms; 1 (shown here) and 2; are
CC produced by alternative splicing.
CC -1- TISSUE SPECIFICITY: Highly expressed in spleen and testis;
CC detected at lower levels in lung and thymus.
CC -1- DISEASE: Defects in TNFRSF13C are a cause of severe B-cell
CC deficiency. B-cell deficient strain A/WySnJ has a 4.7 kb insertion
CC in the BAFFR gene leading to an altered C-terminus. The mutant RNA
CC is not detectable. B-cell lymphoproliferosis is normal, but the life
CC span of peripheral B-cells is much reduced.
CC -1- SIMILARITY: CONTAINS 1 TNFR-CYS REPEAT.
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CC -----
CC EMBL: AF373847; AA01827.1; -.
CC EMBL: AK008142; BAB25490.1; -.
CC MGI: MGI:1919299; Tnfrsf13c.
CC Receptor; Immune response; Signal-anchor; Transmembrane; Glycoprotein;

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KW Alternative splicing. 71 EXTRACELLULAR (POTENTIAL).
 FT DOMAIN 1 71 SIGNAL-ANCHOR (TYPE III MEMBRANE PROTEIN)
 FT TRANSMEM 72 92 (POTENTIAL).
 FT DOMAIN 93 175 CYTOPLASMIC (POTENTIAL).
 FT REPEAT 21 38 TNFR-CYS (PARTIAL).
 FT DISULFID 22 35 BY SIMILARITY.
 FT DISULFID 27 38 BY SIMILARITY.
 FT CARBOHYD 23 23 N-LINKED (GLCNAC...) (POTENTIAL).
 FT VARSPLIC 133 143 MISSING (IN ISOFORM 2).
 SO SEQUENCE 175 AA: 28BCTC1A02EB87EF CRC64;
 Query Match 12.1%, Score 116.5; DB 1; Length 175;
 Best Local Similarity 29.4%; Pred. No. 0.00051;
 Matches 50; Conservative 21; Mismatches 64; Indels 35; Gaps 8;
 QY 7 QCSONEFPLSLHACIPCOL-----RCSNTPPLFCORYCNASVTSYK---GNATL 56
 DB 21 QCNQTCFPLVRCVSCSELPHTPDGTGTSLEGTALQOQBSALRPVALLVCAPIALL 80
 QY 57 WTCLGISLT--ISLAVFVLMFLRKIS---SEPLKDEFKNTGSGLLGMANIDLEKSRGD 111
 DB 81 GILLATLVGLVLSVSMRROOLRTASPDTSSEGVQDE-----SLEWFPVPSSET-- 129
 QY 112 EILPFGLEYVEECTCEDCKSKPKVDSHCFLPAMEGATILVTTT 161
 DB 130 ----PHASAPTPPLK-EDADSALPR-----HSVPVPAITELGSTEIVTTT 170
 RESULT 4
 ID TNFR6_BOVIN STANDARD; PRT: 323 AA.
 AC P51867;
 DT 01-OCT-1996 (Rel. 34, Created)
 DT 01-OCT-1996 (Rel. 34, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Tumor necrosis factor receptor superfamily member 6 precursor (FASL receptor) (Apoptosis-mediating surface antigen FAS) (Apo-1 antigen) (CD95).
 DE TNFRSF6 OR APT1 OR FAS.
 OS Bos taurus (Bovine).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
 OC Bovidae; Bovinae; Bos.
 OX NCBI_TaxID=9913;
 RN (1)
 RP SEQUENCE FROM N.A.
 RX MEDLINE=96226401; PubMed=8634151;
 RA Yoo J., Stone R.T., Beattie C.W.;
 RT "Cloning and characterization of the bovine fas.;"
 RL DNA Cell Biol. 15:227-234(1996).
 CC -1- FUNCTION: Receptor for TNFSF6/FASL. The adaptor molecule FADD recruits caspase-8 to the activated receptor. The resulting death-inducing signaling complex (DISC) performs caspase-8 proteolytic activation which initiates the subsequent cascade of caspases (aspartate-specific cysteine proteases) mediating apoptosis. FAS-mediated apoptosis may have a role in the induction of peripheral tolerance. In the antigen-stimulated suicide of mature T-cells, or both (By similarity).
 CC -1- SUBCELLULAR LOCATION: Type I membrane protein.
 CC -1- DOMAIN: CONTAINS A DEATH DOMAIN INVOLVED IN THE BINDING OF FADD, AND MAYBE TO OTHER CYTOSOLIC ADAPTOR PROTEINS.
 CC -1- SIMILARITY: CONTAINS 3 TNFR-CYS REPEATS.
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 CC -----

DR EMBL: U34794; AAC48546.1; .
 DR HSSP: P25445; IDPF.
 DR InterPro: IPR000488; Death.
 DR InterPro: IPR001368; TNFR_C6.
 DR Pfam: PF00020; TNFR_C6; 3.
 DR Pfam: PF00531; death; 1.
 DR SMART: SM00005; DEATH; 1.
 DR SMART: SM00208; TNFR; 3.
 DR PROSITE: PS00652; TNFR_NGFR_1; 2.
 DR PROSITE: PS00650; TNFR_NGFR_2; 2.
 DR PROSITE: PS50017; DEATH_DOMAIN; 1.
 KW Receptor; Apoptosis; Glycoprotein; Transmembrane; Repeat; Signal.
 FT SIGNAL 1 16
 FT CHAIN 17 323
 FT DOMAIN 17 170
 FT TRANSMEM 171 188
 FT DOMAIN 189 323
 FT REPEAT 45 80
 FT REPEAT 81 124
 FT REPEAT 125 163
 FT DOMAIN 238 306
 FT DISULFID 45 56
 FT DISULFID 57 70
 FT DISULFID 60 79
 FT DISULFID 82 98
 FT DISULFID 101 116
 FT DISULFID 104 124
 FT DISULFID 126 140
 FT DISULFID 143 154
 FT DISULFID 146 162
 FT CARBOHYD 38 38
 FT CARBOHYD 115 115
 SO SEQUENCE 323 AA: 36445 MW: 408849099ELF4892 CRC64;
 Query Match 9.8%; Score 94; DB 1; Length 323;
 Best Local Similarity 22.1%; Pred. No. 0.13;
 Matches 51; Conservative 33; Mismatches 65; Indels 82; Gaps 15;

QY 8 CSQ-NEFPLSLHA--CIPCOL-----RCSN-----T 32
 DB 82 CSEGNVTYTKSHHSKCIKSCDEHGLFEYQCTRTNTKCKSNFPCNSPCEHON 141
 QY 33 PLITCO---RVCNASVNSYKGTNA---ILMTCLGISLTISLAVFVLMFLRKISSEPL 85
 DB 142 PCTTCEHGIIEKCTPTSTNTCKGSRSHANSIMAL---LILLIPILVILIIYKVKSRERNK 197
 QY 86 KDEFKNTGSG---LGMANIDL-----EKSRTGD--EILPFGLEYVEECTCED 130
 DB 198 KNDYCSASASNDGROQLNLTVDGKTYPIAEGMRITVEKFEVRKNGM---EAKIKD 253
 QY 131 CLKSKKRVSDHCFLPAMEGATILVY---TKTDYC---KSLPAALS 173
 DB 254 IMH----DNVH-----ETAEDQVOLLRNWYQSHCKNAVCTLRKSLPKALA 295
 RESULT 5
 ID T13C_HUMAN STANDARD; PRT: 184 AA.
 AC Q96R13;
 DT 15-JUN-2002 (Rel. 41, Created)
 DT 15-JUN-2002 (Rel. 41, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Tumor necrosis factor receptor superfamily member 13C (B cell-activating factor receptor) (BAFF receptor) (BAFF-R) (Blys receptor 3).
 DE TNFRSF13C OR BAFFR OR BR3.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
 OX NCBI_TaxID=9606;
 RN (1)
 RP SEQUENCE FROM N.A. (ISOFORMS 1 AND 2).
 CC -----

FT CONFLICT 844 844 G -> D (IN REF. 2).
 SQ SEQUENCE 867 AA; 97112 MW; D442F6372552B3C8 CRC64;
 Query Match 9.0%; Score 86.5; DB 1; Length 867;
 Best Local Similarity 22.7%; Pred. No. 1.9;
 Matches 44; Conservative 30; Mismatches 67; Indels 53; Gaps 10;
 QY 18 LNAICPOLRCSSNTPITCORNCASVTVNSKGTNAIWTCLGLSLTISLAVFVIMFL 77
 DB 126 LVGCFECMCR-----CNK-CCGEHQRKONAPCRKRCGLSLVLCILMSGLTIV 176
 QY 78 RKSSPLDEKNTGSLGLMANIDLEKSTGDP-ETLL---PRGLTYEECTCE----- 129
 DB 177 GRYANQOTRIKGTOK-----LAKSNRPFQTLLETPQDIDYVEQYNTKNA 227
 QY 130 ---DCIKS-----KPKVSDHCFFLPAMEGATIIIVTK-TNDYCKSLPAAL-- 172
 DB 228 FSDLDIGSVLCGRIKDKLPKRV-----TPVLEIKAMATAIKOKRDALQWMSLSLS 280
 QY 173 ---SATEIKSISA 183
 DB 281 LDAAATQVLTNPLUS 294
 RESULT 7
 FAK2_MOUSE STANDARD; PRT: 1009 AA.
 ID FAK2_MOUSE
 AC 090VP9;
 DT 15-JUN-2002 (Rel. 41, Created)
 DT 15-JUN-2002 (Rel. 41, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Protein tyrosine kinase 2 beta (EC 2.7.1.112) (Focal adhesion kinase
 2) (FAK 2) (Proline-rich tyrosine kinase 2) (Cell adhesion kinase
 beta) (CAK beta) (Calcium-dependent tyrosine kinase) (CADTK) (Related
 adhesion focal tyrosine kinase).
 DE PTK2B OR FAK2 OR PYK2 OR RAFTK.
 GN Mus musculus (Mouse).
 OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 ON NCBI_TaxId=10090;
 RN (1)
 RP SEQUENCE FROM N.A.
 RC TISSUE=Brain;
 RX MEDLINE=96070905; PubMed=7499242;
 RA Avraham S., London R., Fu Y., Ora S., Hilegoudara D., Li J., Jiang S.,
 Pastor L.M., White R.A., Groopman J.E., Avraham H.;
 RT Identification and characterization of a novel related adhesion focal
 tyrosine kinase (RAFTK) from megakaryocytes and brain.*;
 RL J. Biol. Chem. 270:27742-27751(1995).
 RN (2)
 RP PHOSPHORYLATION OF TYR-402, AND INTERACTION WITH NEPHROCYSTIN.
 RX MEDLINE=21396557; PubMed=11493697;
 RA Benning T., Gerke P., Hoepker K., Hildebrandt F., Kim E., Walz G.;
 RT Nephrocytin interacts with Pyk2, p130(Cas), and tensin and triggers
 phosphorylation of Pyk2.*;
 RL Proc. Natl. Acad. Sci. U.S.A. 98:9784-9789(2001).
 CC -1- FUNCTION: Involved in calcium induced regulation of ion channel
 and activation of the map kinase signaling pathway. May represent
 an important signaling intermediate between neuropeptide activated
 receptors or neurotransmitters that increase calcium flux and the
 downstream signals that regulate neuronal activity. Interacts with
 the SH2 domain of Grb2. May phosphorylate the voltage-gated
 potassium channel protein Kv1.2. Its activation is highly
 correlated with the stimulation of c-Jun N-terminal kinase
 activity (By similarity).
 CC -1- CATALYTIC ACTIVITY: ATP + a protein tyrosine - ADP + protein
 tyrosine phosphate.
 CC -1- SUBUNIT: Interacts with Crk-associated substrate (Cas).
 CC Nephrocytin and Grpase regulator associated with FAK (Graf).
 CC SUBCELLULAR LOCATION: Cytoplasmic. Interaction with Nephrocytin
 induces the membrane association of the kinase.
 CC -1- PTM: Phosphorylated on tyrosines in response to various stimuli
 that elevate the intracellular calcium concentration, as well as

by PKC activation. Recruitment by Nephrocytin to cell matrix
 adhesions initiates Tyr-402 phosphorylation. In monocytes,
 adherence to substrata is required for tyrosine phosphorylation
 and kinase activation. Angiostatin II, thapsigargin and L-alpha-
 lysophosphatidic acid (LPA) also induce autophosphorylation and
 increase kinase activity (By similarity).
 CC -1- SIMILARITY: BELONGS TO THE TYR FAMILY OF PROTEIN KINASES. FAK
 SUBFAMILY.
 CC HSSP: P08631; IAD5.
 DR MGD: MGI:104908; Ptk2b.
 DR InterPro: IPR000719; Euk-kinase.
 DR InterPro: IPR005189; Focal_Ar.
 DR InterPro: IPR001245; Tyr-kinase.
 DR Pfam: PF00069; kinase; 1.
 DR Pfam: PF03623; Focal_Ar; 1.
 DR PRINTS: PR00109; TYRKINASE.
 DR ProDom: PD000001; Euk-kinase; 1.
 DR SMART: SM00295; B41; 1.
 DR SMART: SM00219; Tyrc; 1.
 DR PROSITE: PS00107; PROTEIN_KINASE_ATP_1.
 DR PROSITE: PS00011; PROTEIN_KINASE_DOM_1.
 DR PROSITE: PS00109; PROTEIN_KINASE_TYR_1.
 KW Tyrosine-protein kinase; Transferase; ATP-binding; Phosphorylation.
 FT DOMAIN 425 683
 FT NE_BIND 431 439 ATP (BY SIMILARITY).
 FT BINDING 457 457 ATP (BY SIMILARITY).
 FT ACT_SITE 549 549 BY SIMILARITY.
 FT DOMAIN 701 767 PRO-RICH.
 FT DOMAIN 831 869 PRO-RICH.
 FT DOMAIN 868 1009 FOCAL ADHESION TARGETING (FAT).
 FT MOD_RES 402 402 PHOSPHORYLATION.
 FT MOD_RES 579 579 PHOSPHORYLATION (AUTO-) (BY SIMILARITY).
 SQ SEQUENCE 1009 AA; 115821 MW; 963959F656DF9605 CRC64;
 Query Match 8.5%; Score 82; DB 1; Length 1009;
 Best Local Similarity 26.9%; Pred. No. 6;
 Matches 29; Conservative 13; Mismatches 34; Indels 32; Gaps 4;
 QY 88 EFKNTSGGLGNANIDLEKSR-----TGEIILPRGLTYEECTCENDCKSKPRV 138
 DB 249 KEFNT---LAGFANIDQETRYCELIGWNIVDVLPKGIROLTSDFPCTLAFFKQI 305
 QY 139 DSDHCFPLPAME-----EGATIIIVTKTND-----YCK 166
 DB 306 RSIKRLPLETQAVLQLTIEGAPOSTIKTISLAENMADLIDGCR 353
 RESULT 8
 FAK2_RAT STANDARD; PRT: 1009 AA.
 ID FAK2_RAT
 AC P70600; O63201; O88489;
 DT 15-JUL-1998 (Rel. 36, Created)
 DT 15-JUL-1998 (Rel. 36, Last sequence update)
 DE Protein tyrosine kinase 2 beta (EC 2.7.1.112) (Focal adhesion kinase
 2) (FADK 2) (Proline-rich tyrosine kinase 2) (Cell adhesion kinase
 beta) (CAK beta) (Calcium-dependent tyrosine kinase) (CADTK).
 GN Rattus norvegicus (Rat).
 OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 ON NCBI_TaxId=10116;
 RN (1)
 RP SEQUENCE FROM N.A. (ISOFORM 1), AND SEQUENCE OF 310-334; 553-572;
 RP 672-687 AND 989-998.
 RC TISSUE=Liver epithelium;
 RX MEDLINE=97094711; PubMed=6939945;
 RA Yu H., Li X., Marchetto G.S., Dy R., Hunter D., Calvo B., Dawson T.L.,
 Wilk M., Andereg R.J., Graves L.M., Barr H.S.;
 RT Activation of a novel calcium-dependent protein-tyrosine kinase.
 RT Correlation with c-Jun N-terminal kinase but not mitogen-activated
 protein kinase activation.*;
 RL J. Biol. Chem. 271:29993-29998(1996).

RN [2]
 RP SEQUENCE FROM N.A. (ISOFORM 1).
 RC STRAIN-Sprague-Dawley; TISSUE-Brain;
 RA MEDLINE=95403356; PubMed=7673154;
 RX Sasaki H., Nagura K., Ishino M., Tobioke H., Kotani K., Sasaki T.;
 RT "Cloning and characterization of cell adhesion kinase beta, a novel
 protein-tyrosine kinase of the focal adhesion kinase subfamily.";
 RL J. Biol. Chem. 270:21206-21219(1995).
 RM [3]
 RP SEQUENCE FROM N.A. (ISOFORMS 2 AND 3), SUBCELLULAR LOCATION, AND FAT
 RC DOMAIN.
 RC TISSUE-Hippocampus;
 RA MEDLINE=98311659; PubMed=9645946;
 RX Xiong W.-C., Macklem M., Parsons J.T.;
 RT "Expression and characterization of splice variants of PYK2, a focal
 adhesion kinase-related protein.";
 RL J. Cell Sci. 111:1981-1991(1998).
 CC -1- FUNCTION: Involved in calcium induced regulation of ion channel
 and activation of the map kinase signaling pathway. May represent
 an important signaling intermediate between neuropeptide activated
 receptors or neurotransmitters that increase calcium flux and the
 downstream signals that regulate neuronal activity. Interacts with
 the SH2 domain of Grb2. May phosphorylate the voltage-gated
 potassium channel protein Kv1.2. Its activation is highly
 correlated with the stimulation of c-Jun N-terminal kinase
 activity.
 CC -1- CATALYTIC ACTIVITY: ATP + a protein tyrosine -> ADP + protein
 tyrosine phosphate.
 CC -1- SUBUNIT: Isoform 1, but not isoform 2, interacts with crk-
 associated substrate (Cas), Nephrocystin and GTPase regulator
 associated with FAK (Graf).
 CC -1- SUBCELLULAR LOCATION: Cytoplasmic. Interaction with Nephrocystin
 induces the membrane-association of the kinase (by similarity).
 CC Isoform 2 localizes to focal adhesions, but not isoforms 1 and 3.
 CC -1- ALTERNATIVE PRODUCTS: 3 isoforms; 1 (shown here), 2/PKMK and
 3/PYK2s; are produced by alternative splicing.
 CC -1- TISSUE SPECIFICITY: Isoform 1 is expressed at high levels in the
 brain (hippocampus, cerebral cortex and olfactory bulb) and poorly
 expressed in the spleen and other tissues, whereas isoforms 2 and 3 are
 expressed in the spleen and brain (highest in cerebellum).
 CC -1- PTM: Phosphorylated on tyrosines in response to various stimuli
 that elevate the intracellular calcium concentration, as well as
 by PKC activation. Recruitment by Nephrocystin to cell matrix
 adhesions initiates Tyr-402 phosphorylation (by similarity). In
 monocytes, adherence to substrata is required for tyrosine
 phosphorylation and kinase activation. Angiotensin II,
 thapsigargin and L-alpha-lysophosphatidic acid (LPA) also induce
 autophosphorylation and increase kinase activity.
 CC -1- SIMILARITY: BELONGS TO THE TYR FAMILY OF PROTEIN KINASES. FAK
 SUBFAMILY.
 CC
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 or send an email to license@isb-sib.ch).
 CC
 CC EMBL: 069109; AAC52895.1; -
 CC EMBL: DA5854; BAA08290.1; -
 CC EMBL: AF063890; AAC28340.1; -
 CC HSSP: P00523; 2PTK.
 CC InterPro: IPR000719; Euk.pkinase.
 CC InterPro: IPR005189; Focal_AT.
 CC InterPro: IPR001245; Tyr_Pkinase.
 CC Pfam: PF00066; Pkinase_1.
 CC Pfam: PF03623; Focal_AT_1.
 CC ProDom: PD000001; Euk_Pkinase_1.
 CC SMART: SM00295; B41; 1.
 CC SMART: SM00219; TyrcKc_1.
 CC PROSITE: PS00107; PROTEIN_KINASE_ATP; 1.
 CC PROSITE: PS00109; PROTEIN_KINASE_TYR; 1.

DR PROSITE: PS0011; PROTEIN_KINASE_DOM; 1.
 KW Tyrosine-protein kinase; Transferase; Arg-binding; Phosphorylation;
 KM Alternative protein kinase.
 FT DOMAIN 425 683
 FT NP_BIND 431 439
 FT BINDING 457 457
 FT ACT_SITE 549 549
 FT DOMAIN 701 767
 FT DOMAIN 831 869
 FT MOD_RES 868 1009
 FT MOD_RES 402 402
 FT MOD_RES 579 579
 FT VARSPIC 1 771
 FT VARSPIC 772 780
 FT VARSPIC 739 780
 FT CONFLICT 205 205
 FT CONFLICT 807 807
 SQ SEQUENCE 1009 AA; 115784 MM; DA354475BCA49E9B CRC64;
 Query Match 8.5%; Score 82; DB 1; Length 1009;
 Best Local Similarity 26.9%; Pred. No. 6;
 Matches 29; Conservative 13; Mismatches 34; Indels 32; Gaps 4;
 QY 88 EFKNTGSLGMANIDEKSR-----TGCEITLPGLLEYVECECECKSKRPV 138
 DB 249 KEFNT---LAFANIDETRCCLDGMNITVDVIGPGIQLTSODTKPCIAEFKQI 305
 QY 139 DSDHCFPLPAME-----EGATLITVTKTND-----YCK 166
 DB 306 RSIRCLPLEYQVAVLGIGBAPGSLSIKISLAENMADLDICR 353
 RESULT 9
 FAK2_HUMAN STANDARD; PRT; 1009 AA.
 AC 014289; Q16709; Q13475; Q14290;
 DT 15-JUL-1998 (Ref. 36, last sequence update)
 DT 15-JUL-1998 (Ref. 36, last sequence update)
 DT 15-JUN-2002 (Ref. 41, last annotation update)
 DE Protein tyrosine kinase 2 beta (EC 2.7.1.112) (Focal adhesion kinase
 2) (FAK2) (Proline-rich tyrosine kinase 2) (cell adhesion kinase
 beta) (CAK beta) (Calcium-dependent tyrosine kinase) (CAOTK) (Related
 adhesion focal tyrosine kinase).
 GN PTK2B OR FAK2 OR PYK2 OR RAFTK.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 CC Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A. (ISOFORM 1).
 RC TISSUE-Brain;
 RC MEDLINE=95379967; PubMed=7544443;
 RA Lev S., Moreno H., Martinez R., Canoll P., Peles E., Musacchio J.M.,
 RA Ploman G.D., Rudy B., Schlessinger J.;
 RT "Protein tyrosine kinase PYK2 involved in Ca(2+)-induced regulation
 of ion channel and MAP kinase functions.";
 RL Nature 376:737-745(1995).
 RN [2]
 RP SEQUENCE FROM N.A. (ISOFORM 1).
 RC TISSUE-Hippocampus;
 RC MEDLINE=96435932; PubMed=8838818;
 RA Herzog H., Nicholl J., Hort Y.J., Sutherland G.R., Shine J.;
 RT "Molecular cloning and assignment of FAK2, a novel human focal
 adhesion kinase, to 8p11.2-p22 by nonisotopic in situ hybridization.";
 RL Genomics 32:484-486(1996).
 RN [3]
 RP SEQUENCE FROM N.A. (ISOFORM 1).
 RC TISSUE-Hippocampus;
 RC MEDLINE=95403356; PubMed=7673154;
 RX Sasaki H., Nagura K., Ishino M., Tobioke H., Kotani K., Sasaki T.;
 RT "Cloning and characterization of cell adhesion kinase beta, a novel
 protein-tyrosine kinase of the focal adhesion kinase subfamily.";
 RL J. Biol. Chem. 270:21206-21219(1995).

RN [4]
 RP SEQUENCE FROM N.A. (ISOFORM 1).
 RX MEDLINE=96070905; PubMed=7499242;
 RA Avraham S., London R., Fu Y., Ota S., Hiregowdara D., Li J., Jiang S.,
 Pasztor L.M., White R.A., Groopman J.E., Avraham H.;
 RT Identification and characterization of a novel related adhesion focal
 tyrosine kinase (RAFTK) from megakaryocytes and brain.;
 RL J. Biol. Chem. 270:27742-27751(1995).
 RN [5]
 RP SEQUENCE FROM N.A. (ISOFORM 2).
 RC TISSUE=monocytes;
 RX MEDLINE=98211954; PubMed=9545257;
 RA Li X., Hunter D., Morris J., Haskill J.S., Barr H.S.;
 RT "A calcium-dependent tyrosine kinase splice variant in human
 monocytes. Activation by a two-stage process involving adherence and a
 subsequent intracellular signal.";
 RL J. Biol. Chem. 273:9361-9364(1998).
 RN [6]
 RP SEQUENCE FROM N.A.
 RA Blechschmidt K., Jandrig B., Baumgart C., Dettle M.D., Jahn N.,
 RA Menzel U., Schlinabel M.B., Wen G., Taudien S., Rosenthal A.;
 RL Submitted (Oct-2000) to the EMBL/GenBank/DBJ databases.
 RN [7]
 RP PHOSPHORYLATION OF TYR-402, MUTAGENESIS OF PRO-859, AND INTERACTION
 RP WITH NEPHROCYSTIN.
 RX MEDLINE=21396557; PubMed=11493697;
 RA Benning T., Gerke P., Hoepker K., Hildebrandt F., Kim E., Walz G.;
 RT "Nephrocystin interacts with Pyk2, p130(cas), and tensin and triggers
 phosphorylation of Pyk2.";
 RL Proc. Natl. Acad. Sci. U.S.A. 98:9784-9789(2001).
 CC -1- FUNCTION: Involved in calcium induced regulation of ion channel
 and activation of the map kinase signaling pathway. May represent
 an important signaling intermediate between neuropeptide activated
 receptors or neurotransmitters that increase calcium flux and the
 downstream signals that regulate neuronal activity. Interacts with
 the SH2 domain of Grb2. May phosphorylate the voltage-gated
 potassium channel protein Kv1.2. Its activation is highly
 correlated with the stimulation of c-Jun N-terminal kinase
 activity.
 CC -1- CATALYTIC ACTIVITY: ATP + a protein tyrosine -> ADP + protein
 tyrosine phosphate.
 CC -1- SUBUNIT: Interacts with Crk-associated substrate (Cas),
 Nephrocystin and GTPase regulator associated with FAK (Graf).
 CC -1- SUBCELLULAR LOCATION: Cytoplasmic. Interaction with Nephrocystin
 induces the membrane-associated form of the kinase.
 CC -1- ALTERNATIVE PRODUCTS: 2 isoforms; 1 (shown here) and 2; are
 produced by alternative splicing.
 CC -1- TISSUE SPECIFICITY: Most abundant in the brain, with highest
 levels in amygdala and hippocampus. Low levels in kidney. Also
 expressed in spleen and lymphocytes.
 CC -1- PTM: Phosphorylated on tyrosines in response to various stimuli
 that elevate the intracellular calcium concentration, as well as
 by PKC activation. Recruitment by Nephrocystin to cell matrix
 adhesions initiates Tyr-402 phosphorylation. In monocytes,
 adherence to substrata is required for tyrosine phosphorylation
 and kinase activation. Angiotensin II, thapsigargin and L-alpha-
 lysophosphatidic acid (LPA) also induce autophosphorylation and
 increase kinase activity (By similarity).
 CC -1- SIMILARITY: BELONGS TO THE TYR FAMILY OF PROTEIN KINASES. FAK
 SUBFAMILY.
 CC -----
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 CC -----
 DR EMBL: U33284; AAC50203.1; -;
 DR EMBL: L49207; AAB47217.1; -;
 DR EMBL: D45853; BAA08289.1; -;
 DR EMBL: U43522; AAC05330.1; -;

DR EMBL: S80542; AAB35701.1; -;
 DR EMBL: AF311103; -; NOT_ANNOTATED_CDS.
 DR HISSP: P08631; IAD5.
 DR Genew: HGNC:9612; PTK2B.
 DR MIM: 601212; -;
 DR InterPro: IPR000719; Euk_Pkinase.
 DR InterPro: IPR005189; Focal_AT.
 DR InterPro: IPR001245; Tyr_Pkinase.
 DR Pfam: PF00069; Pkinase_1.
 DR Pfam: PF03623; Focal_AT_1.
 DR Prodom: P0000001; Euk_Pkinase_1.
 DR SMART: SM00295; B41; 1.
 DR SMART: SM00219; Tyrc; 1.
 DR PROSITE: PS00107; PROTEIN_KINASE_ATP; 1.
 DR PROSITE: PS00109; PROTEIN_KINASE_TYR; 1.
 DR PROSITE: PS50011; PROTEIN_KINASE_DOM; 1.
 DR Tyrosine-protein kinase; Transferase; ATP-binding; Phosphorylation;
 KM Alternative splicing.
 FT DOMAIN 425 683
 FT NP_BIND 431 439
 FT BINDING 437 457
 FT ACT_SITE 549 549
 FT DOMAIN 702 767
 FT DOMAIN 831 869
 FT DOMAIN 868 1009
 FT MOD_RES 402 402
 FT MOD_RES 578 579
 FT VAR_SEQ 739 780
 FT MOTIF 859 859
 FT FT
 FT CONFLICT 23 23
 FT CONFLICT 256 256
 FT CONFLICT 435 435
 FT CONFLICT 780 780
 SQ SEQUENCE 1009 AA; 115874 MW; 420B21046274E7C2 CRC64;
 Query Match 8.2%; Score 79.5; DB 1; Length 1009;
 Best Local Similarity 32.1%; Pred. No. 10;
 Matches 25; Conservative 9; Mismatches 29; Indels 15; Gaps 3;
 QY 88 EFKNFGSGILGMANIDLEKSR-----TGDEIIPRGLFVECTCEDCIKSKPV 138
 DB 249 KFFNT---LAGRANIDGTYRCGLIGGNITVDLVIGPKIRQLTSQDAKPPICLAEFROI 305
 QY 139 DSDHCPLPLAMEGATIL 156
 DB 306 RSTRICPLT---EEGAVL 320
 RESULT 10
 T13X_HUMAN STANDARD: PRT: 293 AA.
 AC 014836;
 DT 15-JUN-2002 (Rel. 41, Created)
 DT 15-JUN-2002 (Rel. 41, Last sequence update)
 DE Tumor necrosis factor receptor superfamily member 13B (Transmembrane
 DE activator and CAML interactor).
 GN TNFRSF13B OR TACI.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=B-cell;
 RX MEDLINE=97458245; PubMed=9311921;
 RA von Buelow G.-U., Bram R.J.;
 RT "NF-AT activation induced by a CAML-interacting member of the tumor
 RT necrosis factor receptor superfamily.";
 RL Science 278:138-141(1997).
 RN [2]
 RP SEQUENCE FROM N.A.

RC TISSUE=Blood;
 RA Strausberg R.;
 RA Submitted (Apr-2002) to the EMBL/GenBank/DBJ databases.
 RN [3]
 RP FUNCTION.
 RX MEDLINE=20519647; PubMed=10956646;
 RA Wu Y., Bressette D., Carrell J.A., Kaufman T., Feng P., Taylor K.,
 RA Gan Y., Cho Y.H., Garcia A.D., Collatz E., Dimke D., Lapleur D.,
 RA Olsen H.S., Nardelli B., Mel P., Ruben S.M., Ullrich S.J.,
 RA "Tumor necrosis factor (TNF) receptor superfamily member TNFR1 is a
 RT high affinity receptor for TNF family members APRIL and BLys.";
 RL J. Biol. Chem. 275:35478-35485(2000).
 RN [4]
 RP FUNCTION.
 RX MEDLINE=21170294; PubMed=10973284;
 RA Yu G., Boone T., Delaney J., Hawkins N., Kelley M., Ramakrishnan M.,
 RA McCabe S., Qiu W.R., Kornuc M., Xia X.-Z., Guo J., Stolina M.,
 RA Boyle W.J., Sarsai I., Hsu H., Senaldi G., Thell L.E.;
 RT "APRIL and TALL-1 and receptors BCMA and TACI: system for regulating
 RT humoral immunity.";
 RL Nat. Immunol. 1:252-256(2000).
 CC -1- FUNCTION: Receptor for TNFSF13/APRIL and TNFSF13B/TALL1/BAFF/BLys
 CC that binds both ligands with similar high affinity. Mediates
 CC calcineurin-dependent activation of NF-kappa-B, as well as activation
 CC of NF-kappa-B and AP-1. Involved in the stimulation of B- and T-
 CC cell function and the regulation of humoral immunity.
 CC -1- SUBUNIT: Binds TRAF2, TRAF5 and TRAF6. Binds the NH2-terminal
 CC domain of CAMLg with its C-terminus.
 CC -1- SUBCELLULAR LOCATION: Type III membrane protein.
 CC -1- TISSUE SPECIFICITY: Highly expressed in spleen, thymus, small
 CC intestine and peripheral blood leukocytes. Expressed in resting B-
 CC cells and activated T-cells, but not in resting T-cells.
 CC -1- SIMILARITY: CONTAINS 2 TNFR-CYS REPEATS.
 CC -1- CAUTION: It is uncertain whether Met-1 or Met-31 is the initiator.
 CC -----
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 CC -----
 DR EMBL: AF023614; AAC51790.1; -;
 DR EMBL: BC028072; AAH28072.1; -;
 DR Genew: HGNC:18153; TNFRSF13B.
 DR MIM: 604907; -;
 DR InterPro: IPR001368; TNFR_C6.
 DR PROSITE: PS00652; TNFR_NGFR_1; 1.
 DR PROSITE: PS50050; TNFR_NGFR_2; FALSE_NEG.
 KW Receptor; Immune response; Signal-anchor; Transmembrane; Glycoprotein;
 KW Repeat.
 FT DOMAIN 1 165 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 166 186 SIGNAL-ANCHOR (TYPE III MEMBRANE PROTEIN)
 FT CYTOPLASMIC (POTENTIAL).
 FT DOMAIN 187 293
 FT REPEAT 33 67 TNFR-CYS 1.
 FT REPEAT 70 104 TNFR-CYS 2.
 FT DISULFID 34 47 BY SIMILARITY.
 FT DISULFID 50 62 BY SIMILARITY.
 FT DISULFID 54 66 BY SIMILARITY.
 FT DISULFID 71 86 BY SIMILARITY.
 FT DISULFID 89 100 BY SIMILARITY.
 FT DISULFID 93 104 BY SIMILARITY.
 FT CARBOHYD 128 128 N-LINKED (GLCNAC...) (POTENTIAL).
 FT CONFLICT 251 251 P -> L (IN REF. 2).
 SQ SEQUENCE 293 AA; 31816 MW; 411799FDE17A5EB CRC64;

Query Match 8.1%; Score 78.5; DB 1; Length 293;
 Best Local Similarity 19.9%; Pred. No. 3.4;
 Matches 41; Conservative 35; Mismatches 73; Indels 57; Gaps 10;

QY 8 CSQNEFSLHACIPQOLGSSNTPPLTCQRCANASVTSVKGT--NAIIMTCLGLSLI 65
 DB 34 CPEDYWDPLGTGCMSTKTIQHQS--QRTCAACNRLSCRKDGKFFYHLLRDISCAI 92
 QY 66 I-----SLAVEFLMFL-----LRKISSEPLKDFENKTSGLIGMANIDLEKS----- 107
 DB 93 CGQHKKQCAVCEKKNLSPVNLPELRLRQSSGEVENNSNSQR--YQGLEHNGSEASPALP 151
 QY 108 ---RFGDITLLPRG-----LEFYEECTCEDCKISKP-----KVD 139
 DB 152 GKLSADVALVYSTGLCLCAVLCFLVAVACFLKRRDPCOP--RSRPROSPAKSS 209
 QY 140 SDHCFLPLAMEGATILVTTKTDYNC 165
 DB 210 QDH-----AMEAGSPVSTSPRYETC 230

RESULT 11
 YD57_METVA STANDARD; PRT; 343 AA.
 AC Q58752;
 DT 01-NOV-1997 (Rel. 35, Created)
 DT 01-NOV-1997 (Rel. 35, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Putative potassium channel protein MJ1357.
 GN MJ1357.
 OS Methanococcus jannaschii.
 OC Archaea; Euryarchaeota; Methanococci; Methanococcales;
 OC Methanocaldococcaceae; Methanocaldococcus.
 OX NCBI_TaxID=2190;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=JAL-1 / DSM 2661 / ATCC 43067;
 RX MEDLINE=96337999; PubMed=8688087;
 RA Bult C.J., White O., Olsen G.J., Zhou L., Fleischmann R.D.,
 RA Sutton G.G., Blake J.A., Fitzgerald L.M., Clayton R.A., Gocayne J.D.,
 RA Kesteven A.R., Dougherty B.A., Tomb J.-F., Adams M.D., Reisch C.I.,
 RA Scofield R., Kirkness E.F., Weinstock K.G., Merrick J.M., Glodek A.,
 RA Scott J.L., Geoghagen N.S.M., Weidman J.F., Fuhman J.L., Nguyen D.,
 RA Uitterback T.R., Kelley J.M., Peterson J.D., Sadow P.W., Hanna M.C.,
 RA Cotton M.D., Roberts K.M., Hirst M.A., Kaine B.P., Borodovsky M.,
 RA Klenk H.-P., Fraser C.M., Smith H.O., Woese C.R., Venter J.C.;
 RT "Complete genome sequence of the methanogenic archaeon, Methanococcus
 RT jannaschii.";
 RL Science 273:1058-1073(1996).
 CC -1- SUBCELLULAR LOCATION: Integral membrane protein (Potential).
 CC -1- SIMILARITY: STRONG. TO M. JANNASCHII MJ0138.1.
 CC -1- SIMILARITY: TO EUKARYOTIC POTASSIUM CHANNELS.
 CC -----
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 CC -----
 DR EMBL: U67575; AAB99365.1; -;
 DR HSSP: Q54397; 1BL8.
 DR TIGR: MJ1357; -;
 DR InterPro: IPR001622; K+channel_pore.
 DR InterPro: IPR000309; TrkA_KupTake.
 DR InterPro: IPR003148; TrkA_N.
 DR Pfam: PF02080; TrkA-C; 1.
 DR Pfam: PF02254; TrkA-N; 1.
 KW Hypothetical protein; Transmembrane; Transport; Ion transport;
 KW Ionic channel; Complete proteome.
 FT TRANSMEM 8 28
 FT TRANSMEM 30 50 POTENTIAL.
 FT TRANSMEM 62 82 POTENTIAL.
 SQ SEQUENCE 343 AA; 38883 MW; 61231B0C001B54C4 CRC64;

Query Match 8.1%; Score 78.5; DB 1; Length 343;

Best Local Similarity 20.4%; Pred. No. 4;
Matches 39; Conservative 35; Mismatches 66; Indels 51; Gaps 8;

QY 12 EXPDLSLHACIPCOLRGSSNTPPLTCORNCNASTNSVKTNAIMLTCLGLSLISLAVF 71
DB 32 DYFTALFVSIVL-----TITTYGDDFPKPFLLGTLTVLVCVGIVIMLPSL 80
QY 72 VLMLF-----LRKISS--PLKDERKNTGSGLLGMA-----NIDLEKSRIGD 111
DB 81 IAEFLVEGKFEFEVFLKMKKIKTLKDHYITICGYHGLGVGEKFEENIFPIADINE 140
QY 112 EIT-----LRGLEYTVEECTCEDCIKSKPV-----USDICF-PLRAMEBG 152
DB 141 DVLKEBEYKPKPLFYIVGDKNKEEVLR-KAKIDKAGLIATLPDADVFLTLTARELN 199
QY 153 ATILVTTKTNM 163
DB 200 PMLITAKADE 210

RESULT 12
T13X_MOUSE STANDARD: PRT; 249 AA.

ID T13X_MOUSE
AC Q9ERT35; Q9DB23;
DT 15-JUN-2002 (Rel. 41, Created)
DT 15-JUN-2002 (Rel. 41, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Tumor necrosis factor receptor superfamily member 13B (Transmembrane activator and CAML interactor).
GN TNFRSF13B OR TACI.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Splice;
RA MEDLINE=21177254; PubMed=10881172;
RA Yan M., Marsters S.A., Grewal I.S., Wang H., Ashkenazi A., Dixit V.M.;
RT "Identification of a receptor for BlyS demonstrates a crucial role in humoral immunity.";
RL Nat. Immunol. 1:37-41(2000).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Lung;
RA MEDLINE=21085660; PubMed=11217851;
RA Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y., Akazawa T., Hara A., Fukunishi Y., Kono H., Adachi J., Fukuda S., Aizawa K., Iwata M., Nishi K., Kiyosawa H., Kondo S., Yamanaoka I., Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R., Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T., Fleischmann W., Gaasterland T., Giesl C., King B., Kochiba H., Kuehl P., Lewis S., Matsuo Y., Nakai T., Pesole G., Quackenbush J., Schiml L.M., Staahl F., Suzuki R., Tomita M., Wagner L., Washio T., Sakai K., Okido T., Furuno M., Aono H., Balderelli R., Barsh G., Blake J., Borrelli D., Bojunga N., Carninci P., de Bonaldo M.F., Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M., Gustincich S., Hill D., Hofmann M., Hume D.A., Kamuya M., Lee N.H., Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombert P., Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N., Saeki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F., Suzuki H., Toyooka K., Wang K.H., Weitz C., Whitaker C., Wilmink L., Wyman-Horiz A., Yoshida K., Hasegawa Y., Kawai H., Kohitsuki S., Hayashizaki Y.;
RT "Functional annotation of a full-length mouse cDNA collection.";
RL Nature 409:685-690(2001).
RN [3]
RP FUNCTION.
RA MEDLINE=20341628; PubMed=10880535;
RA Xia X.-Z., Treanor J., Senaldi G., Khare S.D., Boone T., Kelley M., Theill L.E., Colombero A., Solovayev I., Lee F., McCabe S., Elliott R., Miner K., Hawkins N., Guo J., Stolina M., Yu G., Wang J., Delaney J.,

RA Meng S.-Y., Boyle W.J., Han H.;
RT "TACI is a TRAF-interacting receptor for TALL-1, a tumor necrosis factor family member involved in B cell regulation.";
RL J. Exp. Med. 192:137-143(2000).
RN [4]
RP FUNCTION.
RX MEDLINE=21322748; PubMed=11429548;
RA Yan M., Marsters S.A., Baker T., Chan B., Lee W.P., Fu L., Tumas D., Wang H., Dixit V.M., Ashkenazi A., Grewal I.S.;
RT "TACI-ligand interactions are required for T cell activation and collagen-induced arthritis in mice.";
RL Nat. Immunol. 2:632-637(2001).
CC -1- FUNCTION: Receptor for TNFSF13/APRIL and TNFSF13B/TALL1/BAPF/BLYS that binds both ligands with similar high affinity. Mediates calcineurin-dependent activation of NF-AT, as well as activation of NF-kappa-B and AP-1. Involved in the stimulation of B- and T-cell function and the regulation of humoral immunity (By similarity).
CC -1- SUBUNIT: Binds TRAF2, TRAF5 and TRAF6. Binds the NH2-terminal domain of CAML with its C-terminus (by similarity).
CC -1- SUBCELLULAR LOCATION: Type III membrane protein (probable).
CC -1- SIMILARITY: CONTAINS 2 TNFR-CYS REPEATS.
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CC
DR EMBL; AF257673; AAC00081.1; -;
DR EMBL; AK004668; BAB23457.1; -;
DR GDB; MGI:1889411; TNfrsf13b.
DR PROSITE; PS00652; TNFR-NGFR_1; 1.
DR PROSITE; PS50050; TNFR-NGFR_2; 2.
KW Receptor; Immune response; Signal-anchor; Transmembrane; Repeat.
FT DOMAIN 1 128
FT SIGNAL-ANCHOR (POTENTIAL).
FT TRANSMEM
FT 129 149
FT DOMAIN 150 249
FT REPEAT 5 38
FT REPEAT 42 76
FT DISULFID 6 19
FT DISULFID 22 34
FT DISULFID 26 38
FT DISULFID 43 58
FT DISULFID 61 72
FT DISULFID 65 76
FT CONFLICT 137 137
SQ SEQUENCE 249 AA; 26947 MW; CBZF2D6IC2931D81 CRC64;

Query Match 8.0%; Score 77; DB 1; Length 249;
Best Local Similarity 21.7%; Pred. No. 3.9;
Matches 43; Conservative 21; Mismatches 70; Indels 64; Gaps 11;

QY 10 ONEYPSLHACIPCOLRGSSNTPPLTCORNCNASTNSVKTNAIMLTCLGLSLISLAVF 53
DB 47 QGRYDHLHAGVSDSDSTCTQH--PQCAHRCCEKRRSQNMQLPELGRQAGEVEVRSDN 104
QY 54 A-----LWMTCLGLSLISLAVLV---MFLRKISSPELKDERN 91
DB 105 SCRHOGEHGPGLRLSSDQLTYCTLGVCCALIFCCFLVALASFLRR--GBPLPSQAPG 162
QY 92 TCGSLGLMANIDLEKSRFGDITL-PRGLETYVEECTCEPCI-----KKPKYVSDN 142
DB 163 PRGSOANSPHARPYTEACDEVTASQPVE-----TCSRCFERNSSPTGDSAPRSLDII 216
QY 143 CF-----PLPAMEGATI 155
DB 217 GFAGTAAPQPCMR--ATV 232

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RESULT 13
YCSB_SCHPO STANDARD; PRT: 638 AA.
ID YCSB_SCHPO
AC 074910;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Hypothetical WD-repeat protein C613.12c in chromosome III.
GN SPC613.12C.
OS Schizosaccharomyces pombe (fission yeast).
OC Eukaryota; Fungi; Ascomycota; Schizosaccharomycetes;
OC Schizosaccharomycetales; Schizosaccharomycetaceae;
OC Schizosaccharomycetes;
OX NCBI_TaxID=4896;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=972;
RX MEDLINE=21849401; PubMed=11859360;
RA Wood V., Gwilliam R., Rajandream M.A., Lyne M., Lyne R., Stewart A.,
RA Sgouros J., Peat N., Hayles J., Baker S., Basham D., Bowman S.,
RA Brooks K., Brown D., Brown S., Chillingworth T., Churcher C.M.,
RA Collins M., Connor R., Cronin A., Davis P., Feltwell T., Fraser A.,
RA Gentles S., Goble A., Hamlin N., Harris D., Hidalgo J., Hodson G.,
RA Holtroyd S., Hornsby T., Howarth S., Huckle E.J., Hunt S., Jagsels K.,
RA James K., Jones L., Jones M., Leather S., McDonald S., McLean J.,
RA Mooney P., Moule S., Mungall K., Murphy L., Niblett D., Odeh C.,
RA Oliver K., O'Neill S., Pearson D., Quail M.A., Rabinowitsch E.,
RA Rutherford K., Rutter S., Saunders D., Seeger K., Sharp S.,
RA Skelton J., Simmonds M., Squares R., Squares S., Stevens K.,
RA Taylor K., Taylor R.G., Tivey A., Walsh S.V., Warren T., Whitehead S.,
RA Woodward J., Volkert G., Aert R., Robben J., Gymnopoulos B.,
RA Wellings I., Vanstreels E., Rieger M., Schaefer M., Mueller-Auer S.,
RA Gabel C., Fuchs M., Fritz C., Holzner E., Moestl D., Hildert H.,
RA Borzym K., Langer M., Beck A., Leinach H., Reinhardt R., Pohl T.M.,
RA Eger P., Zimmermann W., Medler H., Wandtke R., Punelle B.,
RA Goffeau A., Cadieu S., Dreano S., Gloux S., Lelaie V., Mottier S.,
RA Galibert F., Ayres S.J., Xiang Z., Hunt C., Moore K., Hurst S.M.,
RA Lucas M., Rochet M., Galliard J., Tallada V.A., Garzon A., Rhode G.,
RA Dada R.R., Cruzado L., Jimenez J., Sanchez M., del Rey F., Benito J.,
RA Dominguez A., Revuelta J.L., Moreno S., Armstrong J., Forsburg S.L.,
RA Cerrutti L., Lowe T., McCombie W.R., Paulsen I., Potashkin J.,
RA Shpakovski G.V., Uesery D., Barrell B.G., Nurse P.;
RL *The genome sequence of Schizosaccharomyces pombe.*;
RL Nature 415:871-880(2002).
CC -! SIMILARITY: CONTAINS 4 WD REPEATS (TRP-ASP DOMAINS).
CC -!
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CC -----
CC EMBL: AL011644; CAA21064.1;
CC InterPro: IPR001680; WD40.
CC Pfam: PF00400; WD40. 4.
CC PRINTS: PR00320; GPROTEINDRPT.
CC SMART: SM00320; WD40. 4.
CC PROSITE: PS00678; WD_REPEATS_1; 2.
CC PROSITE: PS00682; WD_REPEATS_2; 2.
CC PROSITE: PS50294; WD_REPEATS_REGION; 1.
CC Hypothetical protein; Repeat; WD repeat.
CC REPEAT 297 336 WD 1.
CC REPEAT 486 525 WD 2.
CC REPEAT 544 583 WD 3.
CC REPEAT 587 626 WD 4.
CC SEQUENCE 638 AA; 71536 MW; 6CD3608748AAFP98 CRC64;
Query Match 7.8%; Score 75.5; DB 1; Length 638;
Best Local Similarity 22.7%; Pred. No. 15;
Matches 44; Conservative 20; Mismatches 61; Indels 69; Gaps 7;

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OY 12 EYFDSLHACIPOLCRSSNTPPLTCORCNASVTSYKGTNAIITGLISLAVF 71
DB 42 ELYDFYRAELPCP-----KPSLSISKSHIAKVPNSVNRK-----LEIOLLTSGTF 88
OY 72 VLMFLRKISSEPLKDEFKRTNGSGLGMANIDKESRTGDEILPGLGEYEEC----- 126
DB 89 L-----PNSRPLTSEVRKHTL-----LSNITDDKRPSLIHDFTEECFIIQE 134
OY 127 -----TCEDCIKSKPVYSDHCPLPAEEGATILVT 158
DB 135 AKLKEGPVNSVQFNDAYSTHISPLPRAYEDC-----QKEFDINPSLSVPKRGHAIILRT 190
OY 159 TKTN-----DYCKS 167
DB 191 YKKNKKLLPDYLS 204
RESULT 14
SRK6_BRAOL STANDARD; PRT: 849 AA.
ID SRK6_BRAOL
AC 009092;
DT 01-FEB-1995 (Rel. 31, Created)
DT 01-FEB-1995 (Rel. 31, Last sequence update)
DT 01-NOV-1995 (Rel. 32, Last annotation update)
DE Putative serine/threonine kinase receptor precursor (EC 2.7.1.37)
DE (S-receptor kinase) (SRK).
GN SRK6.
OS Brassica oleracea (Cauliflower).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eustos II; Brassicales; Brassicaceae; Brassica.
OX NCBI_TaxID=3712;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=CV. S6S6; TISSUE=Stigma;
RX MEDLINE=92020942; PubMed=1681543;
RA Stein J.C., Howlett B., Boyes D.C., Nasrallah M.E.;
RT *Molecular cloning of a putative receptor protein kinase gene encoded
RT at the self-incompatibility locus of Brassica oleracea.*;
RL Proc. Natl. Acad. Sci. U.S.A. 88:8815-8820(1991)
CC -! FUNCTION: INVOLVED IN SPOROPHYTIC SELF-INCOMPATIBILITY SYSTEM
CC (THE INABILITY OF FLOWERING PLANTS TO ACHIEVE SELF-
CC FERTILIZATION), PROBABLY ACTING IN COMBINATION WITH S-LOCUS-
CC SPECIFIC GLYCOPROTEINS. INTERACTION WITH A LIGAND IN THE
CC EXTRACELLULAR DOMAIN TRIGGERS THE PROTEIN KINASE ACTIVITY OF THE
CC CYTOSOLIC DOMAIN.
CC -! CATALYTIC ACTIVITY: ATP + a protein - ADP + a phosphoprotein.
CC -! SUBCELLULAR LOCATION: Type I membrane protein.
CC -! TISSUE SPECIFICITY: PREDOMINANTLY IN THE PISTIL AND ANTHER.
CC -! POLYMORPHISM: THERE ARE A NUMBER OF DIFFERENT S ALLELES IN
CC B. OLERACEA, POSSIBLY PROVIDING THE RECOGNITION SPECIFICITY.
CC -! SIMILARITY: THE EXTRACELLULAR DOMAIN IS SIMILAR TO S-LOCUS
CC GLYCOPROTEINS OF BRASSICA, WHILE THE INTRACELLULAR DOMAIN IS
CC A SER/THR-PROTEIN KINASE RELATED TO RAF KINASES.
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CC -----
CC EMBL: M76647; AAA33000.1; ATL-TERM.
CC InterPro: IPR001480; B_lectin..
CC InterPro: IPR000719; Euk_Dkinase.
CC InterPro: IPR003609; Pan_app.
CC InterPro: IPR004040; STY_Pkinase.
CC InterPro: IPR002290; Ser_thr_Pkinase.
CC InterPro: IPR000858; Slocus_glycop.
CC Pfam: PF00069; Pkinase; 1.
CC Pfam: PF00954; Slocus_glycop; 1.
CC Pfam: PF01453; Agglutinin; 1.

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DR Prodom: P000001; Euk.pkinase.1.
 DR SMART: SM00108; B.lectin.1.
 DR SMART: SM00473; PAN.Ap.1.
 DR SMART: SM00221; STKG.1.
 DR PROSITE: PS00107; PROTEIN_KINASE_ATP.1.
 DR PROSITE: PS00108; PROTEIN_KINASE_ST.1.
 DR PROSITE: PS50011; PROTEIN_KINASE_DOM.1.
 KW Transferrase; Serine/threonine-protein kinase; Signal; ATP-binding;
 KW Transmembrane; Receptor; Glycoprotein; Self-incompatibility.
 FT SIGNAL 1 32
 FT CHAIN 33 849
 FT PUTATIVE SERINE/THREONINE KINASE
 FT RECEPTOR.
 FT EXTRACELLULAR (POTENTIAL).
 FT POTENTIAL.
 FT CYTOPLASMIC (POTENTIAL).
 FT PROTEIN KINASE.
 FT NP_BIND 534 542
 FT ATP (BY SIMILARITY).
 FT BINDING 556 556
 FT ATP (BY SIMILARITY).
 FT ACT_SITE 653 653
 FT BY SIMILARITY.
 FT CARBOHYD 47 47
 FT N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 120 120
 FT N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 196 196
 FT N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 260 260
 FT N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 314 314
 FT N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 389 389
 FT N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 442 442
 FT N-LINKED (GLCNAC. . .) (POTENTIAL).
 SQ SEQUENCE 849 AA; 97231 MW; 7E156059EDDF4370 CRC64;

Query Match 7.88; Score 75; DB 1; Length 849;
 Best Local Similarity 17.68; Pred. No. 23;
 Matches 33; Conservative 30; Mismatches 50; Indels 74; Gaps 7;

OY 24 COLRSSNTPPLTCORYNASVTSVKGTNALWT----- 58
 DB 380 CKKRTSD--CNCFAFMANDIRNG--GSGCVITRLEDIRNYATDAIDGDLVRLAA 434
 OY 59 -----CGLSLIISLAVFVLMFLRKISSEPLKDEKNTGSLGMANIDLEK 106
 DB 435 ADIAKRRNAGKISLTLYGVSALLLMFCL-----WKRKORAKASISIANTORNO 487
 OY 107 SRTGDEIILPRLGLEYVECTCEDCIKSRKPVSDHCF-----PLPAMEGATILVTTKT 161
 DB 488 NLPMEVTL-----SSKREFGEYKFEELPLLEME---TVVKATEN 527
 OY 162 NDYCKSL 168
 DB 528 FSSCNKL 534

RESULT 15
 EROI_KLULA STANDARD; PRT; 384 AA.
 AC P41771.
 DT 01-NOV-1995 (Rel. 32, Created)
 DT 01-NOV-1995 (Rel. 32, Last sequence update)
 DT 01-NOV-1995 (Rel. 32, Last annotation update)
 DE EROI protein.
 GN EROI.
 OS Kluyveromyces lactis (Yeast).
 OC Saccharomycetes; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
 OC Saccharomycetales; Saccharomycetaceae; Kluyveromyces.
 OX NCBI_TaxID=28985;
 RN 11
 RP SEQUENCE FROM N.A.
 RX MEDLINE=95084639; PubMed=7992512;
 RA Dean N.;
 RT "Cloning and DNA sequence of a Kluyveromyces lactis EROI homologue."
 RL Yeast 10:1117-1124(1994)
 CC -1- FUNCTION: REQUIRED FOR THE RETENTION OF LUMINAL ENDOPLASMIC
 CC RETICULUM PROTEINS. AFFECTS GLYCOPROTEIN PROCESSING IN THE
 CC GOLGI APPARATUS.
 CC -1- SUBCELLULAR LOCATION: Integral membrane protein.
 CC -----

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 CC -----
 DR EMBL: U04714; AAA21530.1; -
 DR InterPro: IPR004342; EXS_Cterm.
 DR Pfam: PF03124; EXS; 1.
 KW Endoplasmic reticulum; Transmembrane; Protein transport.
 FT TRANSMEM 19 36
 FT POTENTIAL.
 FT TRANSMEM 78 94
 FT POTENTIAL.
 FT TRANSMEM 102 123
 FT POTENTIAL.
 SQ SEQUENCE 384 AA; 45315 MW; C064F9A67C96845B CRC64;

Query Match 7.78; Score 74.5; DB 1; Length 384;
 Best Local Similarity 27.28; Pred. No. 11;
 Matches 43; Conservative 21; Mismatches 55; Indels 39; Gaps 8;

OY 9 SONEYFDSLHACIPQQLRCSNTPPLTCORYNASVTSVKGTNALIWTGIGLSIISL 68
 DB 67 SSKLKFSSISRYIIPWQVLC-----IILFOY--SFTNNV--SNKLWFLNVSPLLEL 115
 OY 69 AVFVLMFLRKISSEPLKDEKNTGSLGMANIDLEKSTGDEIILPRLGLEYVECTC 128
 DB 116 -FYIFAMILR--SSAMVACFRK---ILWVADIEPPKRYNNYIISDPLTSY----- 161
 OY 129 EDCIKSRKPVSDHCFPLPAMEGATILVTTKTNDYCK 166
 DB 162 -----SKPLVD-----LAIVATFLFHDPTVKQK 185

Search completed: November 12, 2002, 16:58:58
 Job time : 17.794 secs

097D61 PRELIMINARY; PRT: 217 AA.
 AC Q97D61;
 DT 01-OCT-2001 (TrEMBLrel. 18, Created)
 DT 01-OCT-2001 (TrEMBLrel. 18, last sequence update)
 DT 01-DEC-2001 (TrEMBLrel. 19, last annotation update)
 DE Amino acid ABC transporter, permease component.
 GN CAC3619.
 OS Clostridium acetobutylicum.
 OC Bacteria; Firmicutes; Bacillus/Clostridium group; Clostridia;
 OC Clostridiales; Clostridiaceae; Clostridium.
 CX NCBI_TaxID=1488;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=ATCC 824 / DSM 792 / VKM B-1787;
 RX MEDLINE=21359325; PubMed=1466286;
 RA Noelling J., Breton G., Omelchenko M.V., Makarova K.S., Zeng Q.,
 RA Gibson R., Lee H.M., Dubois J., Qiu D., Hittl J., Wolf Y.T.,
 RA Tatusov R.L., Sabathe F., Doucette-Stamm L., Soucaille P., Daly M.J.,
 RA Bennett G.N., Koonin E.V., Smith D.R.;
 RT "Genome sequence and comparative analysis of the solvent-producing
 RT bacterium Clostridium acetobutylicum."
 RL J. Bacteriol. 183:4823-4838(2001).
 DR EMBL: AE007858; AAK81542.1;
 DR InterPro: IPR000515; BPD.transp.
 DR Pfam: PF00528; BPD.transp. 1.
 DR PROSITE: PS00402; BPD_TRANSF_INN_MEMBERS: 1.
 KW Complete proteome.
 SQ SEQUENCE 217 AA; 23743 MW; 36738BCDCDE8A2P CRC64;

Query Match 9.2%; Score 88.5; DB 16; Length 217;
 Best Local Similarity 24.8%; Pred. No. 0.25;
 Matches 55; Conservative 25; Mismatches 77; Indels 65; Gaps 10;

QY 16 SLINACTPCQLRCSSNTPPLTCORCYCNASY-----TNSVKNTAI-----LMTCLGL 62
 DB 4 SLKLVVPLVDGRTIRITLLTGSSITIGCITIAMFKTSSVKLVNIGKFTWILNGT 63
 QY 63 SLISLAVFV--LMFLRKISSEPLKDEF-----KNTGS-----GLIGMANIDLEKSR 108
 DB 64 PLILQIVVYVGGPFLSDKLTMTPKMAALIGLSNGAVIATIRINGITLAINQGFESK 123
 QY 109 -----TGDEITLPFGLEYVEEC-----TEEDCI-KSKRVSDH 142
 DB 124 ALGLTGTGTMKRITLPAIRVAVIPGCGNEFIAMIKDTSLVSVITWEEELRAQLLVSSG 183
 QY 143 CFPPLAMEGA--TILVTTKNDYCKSLPALSAIEIKSIS 182
 DB 184 DAVTPYLFAGIFVILITFTPTGFESK-----IERKLS 215

RESULT 3

QY 08R056 PRELIMINARY; PRT: 842 AA.
 AC Q8R056;
 DT 01-JUN-2002 (TrEMBLrel. 21, Created)
 DT 01-JUN-2002 (TrEMBLrel. 21, last sequence update)
 DT 01-JUN-2002 (TrEMBLrel. 21, last annotation update)
 DE Hypothetical 94.5 kDa protein.
 OS Mus musculus (Mouse).
 OC Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 CX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=EYE;
 RA Strausberg R.;
 RL Sumitted (Apr-2002) to the EMBL/GenBank/DBJ databases.
 DR EMBL: BC028286; AAH28286.1;
 KW Hypothetical protein.
 SQ SEQUENCE 842 AA; 94478 MW; 734C10D715E5B9C2 CRC64;

Query Match 9.0%; Score 86.5; DB 11; Length 842;

Best Local Similarity 22.7%; Pred. No. 1.9;
 Matches 44; Conservative 30; Mismatches 67; Indels 53; Gaps 10;
 QY 18 LHACIPCOLRCSSNTPPLTCORCYCNASYKGTNAIMTCLGLSLISLAVFL 77
 DB 126 LVGCFPCMCRC-----CNK-CGEMHOKRONAPCRKCLGLSLIVCLIMSLGIY 176
 QY 78 RKISSEPLKDEFKNTGSLGMANIDLEKSRGD--EIL--PRLETVEEC----- 129
 DB 177 GFVAHQTRTRIKGTOK-----LAKSNRDRQTLTTPPKQIDIVVQYTRTKKA 227
 QY 130 ---DCIKS-----KRVSDHCFPLAMEGATILVTV--TNDYCKSLPAL-- 172
 DB 228 FSDLDIGISVVGRIKDKLPKV-----TPVLEEIKAMATAIKQTFDALQNMSSSIKS 280
 QY 173 ---SATEIKSISA 183
 DB 281 LQDAAQTQNTUUS 294

RESULT 4

QY1X8

ID QY1X8 PRELIMINARY; PRT: 1193 AA.
 AC QY1X8;
 DT 01-NOV-1999 (TrEMBLrel. 12, Created)
 DT 01-MAR-2002 (TrEMBLrel. 20, last sequence update)
 DT 01-JUN-2002 (TrEMBLrel. 21, last annotation update)
 DE Protein tyrosine kinase.
 GN EPPK178.
 OS Ephydrelia fluviatilis.
 OC Eukaryota; Metazoa; Porifera; Demospongiae; Ceractinomorpha;
 OC Haplosclerida; Spongillidae; Ephydrelia.
 CX NCBI_TaxID=31330;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=99246375; PubMed=10229568;
 RA Suga H., Koyanagi M., Hoshiyama D., Ono K., Iwabe N., Kuma K.,
 RA Miyata T.;
 RT "Extensive gene duplication in the early evolution of animals before
 RT the parazoan-eumetazoan split demonstrated by G proteins and protein
 RT tyrosine kinases from sponge and hydrate."
 RL J. Mol. Evol. 48:646-653(1999).
 RN [2]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=21601119; PubMed=11738833;
 RA Suga H., Katoh K., Miyata T.;
 RT "Sponge homologs of vertebrate protein tyrosine kinases and frequent
 RT domain shufflings in the early evolution of animals before the
 RT parazoan-eumetazoan split."
 RL Gene 280:195-201(2001).
 DR EMBL: AB006570; BAB81724.2;
 DR HSBP: P08631; IADS.
 DR InterPro: IPR000494; EGFR_L_domain.
 DR InterPro: IPR000719; Euk-kinase.
 DR InterPro: IPR002174; Furin-lik.
 DR InterPro: IPR002290; Ser_thr-kinase.
 DR InterPro: IPR001368; TNFR-c6.
 DR InterPro: IPR001245; Tyr-kinase.
 DR Pfam: PF00757; Furin-likel. 1.
 DR Pfam: PF00063; kinase. 1.
 DR Pfam: PF01030; Recep_L_domain. 2.
 DR PRINTS: PR00109; TYRKINASE.
 DR ProDom: PD000001; Euk-kinase; 2.
 DR SMART: SM00261; FU; 6.
 DR SMART: SM00220; STKC; 1.
 DR SMART: SM00219; TYRK; 1.
 DR PROSITE: PS00107; PROTEIN_KINASE_ATP; 1.
 DR PROSITE: PS00111; PROTEIN_KINASE_DOM; 1.
 DR PROSITE: PS00109; PROTEIN_KINASE_TYR; 1.
 DR PROSITE: PS00652; TNFR_NGFR_1; UNKNOWN_1.
 KW Kinase.
 SQ SEQUENCE 1193 AA; 128169 MW; 009E4AC9BC12DF60 CRC64;


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Query Match Similarity      8.9%: Score 85.5; DB 5; Length 1193;
Best Local Similarity      22.3%: Pred. No. 3.6;
Matches      37; Conservative      28; Mismatches      56; Indels      45; Gaps      8;

OY      2 LONAGCCSONEYFDSLILACIPQOLRCSSNTPP----LTCQRYCNASVTVNSVKGATNAL 56
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB      715 LCVSGSNDTEYODALN-CLTPCANGCIGCGSGPISQCLTCA--SGSCCTTVDOSSGGII 771
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :

OY      57 WPCGLSLIISLA--VFVLMFLRKISSEPLKCFEKNCTSGSLGMANIDLEKSRGDEI 113
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB      772 GIVFGSIVVIFLATISVILFLYIRRYRHKFKFRKRSTOA---MCSN-----GNET 820
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :

OY      114 ILPRGLEVEVEECTCEDCKSRKPVSDH---CFPLPMEGATGI 155
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB      821 LRP-----PKLPDPATRLITPPTALEOGQVL 847
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :

RESULT 5
O98RW7      PRELIMINARY; PRT; 938 AA.
AC      O98RW7;
DT      01-JUN-2002 (TREMBLrel. 21, Created)
DT      01-JUN-2002 (TREMBLrel. 21, Last sequence update)
DT      01-JUN-2002 (TREMBLrel. 21, Last annotation update)
DE      Hypothetical 103.6 kDa protein.
OS      Arabidopsis thaliana (Mouse-ear cress).
OC      Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC      Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC      eurosids II; Brassicales; Brassicaceae; Arabidopsids.
OX      NCBI_TaxID=3702;
RN      [1]
RP      SEQUENCE FROM N.A.
RA      Yamada K., Banb J., Chan M.M., Chang C.H., Chang E., Dale J.M.,
RA      Dang J.M., Goldsmith A.D., Lee J.M., Onodera C.S., Quach H.L.,
RA      Tang C., Toriumi M., Wu H.C., Yamamura Y., Yu G., Bowser L.,
RA      Garofanci P., Chen H., Cheuk R., Hayashizaki Y., Ishida J., Jones T.,
RA      Kamiya A., Karlin-Neumann G., Kawai J., Kim C., Lam B., Lin J.,
RA      Meyers M.C., Miranda M., Narusaka M., Nguyen M., Palm C.J.,
RA      Sakurai T., Sakou M., Seki M., Shino P., Southwick A., Shinozaki K.,
RA      Davis R.W., Ecker J.R., Theologis A.;
RT      "Arabidopsis full length cDNA clones.";
RT      Submitted (MAR-2002) to the EMBL/GenBank/DBJ databases.
DR      EMBL, AY091078; AM13898.1; -.
KW      Hypothetical protein.
SQ      SEQUENCE      938 AA; 103602 MW; 3E78395D65D75C95 CRC64;

Query Match      8.7%: Score 83.5; DB 10; Length 938;
Best Local Similarity      29.4%: Pred. No. 4.5;
Matches      37; Conservative      18; Mismatches      28; Indels      43; Gaps      9;

OY      38 ORCNASVTVNSVGTNAIIMFCGLSLIISLAIVYLMFLRKISSEPLK-EPKN--TGS 94
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB      29 ERYCSA--NSALGTPSM--C-----SSTGPFQDSERFENSLGP 62
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :

OY      95 GLGMANIDLEKSRDEITLPRGLEVEVEECTCEDCKSRP-----KVSDHCFLPLPAM 149
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB      63 SLVYLSLSDW--SRLDG-----RGHIFDEGSGCNGRESSAPGLNTGVNIDMCQGL-M 113
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :

OY      150 EEGATI 155
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB      114 DGGATI 119
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :

RESULT 6
O98TR8      PRELIMINARY; PRT; 1998 AA.
AC      O98TR8;
DT      01-MAY-2000 (TREMBLrel. 13, Created)
DT      01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DT      01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DE      Hypothetical 223.5 kDa protein.
GN      T24C20_80.

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OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC euroids II; Brassicales; Brassicaceae; Arabidopsids.
OX NCBI_TaxID=3702;
RN [1]
RP SEQUENCE FROM N.A.
RA Choinsne N., Robert C., Brottier P., Mincker P., Catolico L.,
RA Attienuevau F., Saurin W., Weissenbach J., Mewes H.W., Rudd S.,
RA Lemcke K., Mayer K.F.X., Queller F., Salanoubat M.;
RL Submitted (JUL-1999) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RA EU Arabidopsis sequencing project;
RL Submitted (May-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL: AL096856; CAB51067.1;
DR InterPro: IPR000515; BPD_transp.
DR Interpro: IPR001683; PX.
DR Pfam: PF00787; PX.1
DR SMART: SM00312; PX.1
DR PROSITE: PS00402; BPD_TRANSF_INN_MEMBER; UNKNOWN.1.
KW Hypothetical protein.
SQ SEQUENCE 1998 AA: 223513 MW: 8B3D6A03CD24BF55 CRC64;

Query Match      8.7% Score 83.5; DB 10; Length 1998;
Best Local Similarity 29.4%; Pred. NO. 11;
Matches 37; Conservative 18; Mismatches 28; Indels 43; Gaps 9.

QY 38 ORYCNASVTNSVKGNALIMTCLGLSLIISIAVFLMFLRKISSPLKD-EKKN--TGS 94
Db 1089 ERYCSA---NSALGTPSM---C-----SSTGFQDSFEFNESILGP 1122
          :|::||| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::|
QY 95 GLICMANIDEKERDELLIPRGLEYVEECTCEDCIKSKP-----KYSDHCFFLPAPW 149
Db 1123 SLVNLSSLDLW-SRLDD-----RGHIFPEGSGSCNGRASSAPGLANTGVNIIDNCGLD-N 1173
          ||::|::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::|
QY 150 EGCGATI 155
Db 1174 DGGATI 1179
          :|||

RESULT 7
O97491 PRELIMINARY; PRT: 327 AA.
ID O97491
AC O97491;
DT 01-MAY-1999 (TrEMBLrel_10, Created)
DT 01-MAY-1999 (TrEMBLrel_10, Last sequence update)
DT 01-JUN-2001 (TrEMBLrel_17, Last annotation update)
DE Fas protein.
GN Fas.
OS Ovis aries (Sheep).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Caprinae; OVAs.
OX NCBI_TaxID=9940;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE-LYMPHOCTE;
RA Takagi M., Takahashi H., Kabeya H., Ohashi K., Sugimoto C., Onuma M.;
RL Submitted (MAR-1998) to the EMBL/GenBank/DBJ databases.
DR EMBL: AB01671; BA037093.1;
DR HSSP: P25445; IDDF.
DR InterPro: IPR000488; Death.
DR Interpro: IPR001368; TNFR_c6.
DR Pfam: PF00531; death.1.
DR Pfam: PF00020; TNFR_c6; 3.
DR SMART: SM00005; DEATH; 1.
DR SMART: SM00208; TNFR; 3.
DR PROSITE: PSS0017; DEATH_DOMAIN; 1.
DR PROSITE: PS00652; TNFR_NGR_1; 1.
DR PROSITE: PSS0050; TNFR_NGR_2; 2.
SQ SEQUENCE 327 AA: 36928 MW: 5CFEE84AB2BE387A CRC64;

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[illegible]

QY	177	LEKS	180	
DB	362	IDON	365	
RESULT 12				
081820				
ID	081820	PRELIMINARY;	PRT;	735 AA.
AC	081820			
DT	01-NOV-1998 (TREMblrel. 08	Created)		
DT	01-NOV-1998 (TREMblrel. 08	Last sequence update)		
DT	01-MAR-2002 (TREMblrel. 20	Last annotation update)		
DE	WALL-associated kinase 1 (putative wall-associated kinase 1).			
GN	WAK1 OR F16F4.6.			
OC	Arabidopsis thaliana (Mouse cross).			
OC	Eukaryota: Viridiplantae: Streptophyta: Embryophyta: Tracheophyta:			
OC	Spermatophyta: Magnoliophyta: eudicotyledons: core eudicots: Rosidae:			
OC	eurosidia II: Brassicales; Brassicaceae; Arabidopsis.			
OX	NCBI_TaxID=3702;			
XX	[1]			
RE	SEQUENCE FROM N.A.			
RE	MEDLINE-99308512; Pubmed-10380805;			
RA	He Z. H., Cheeseman I., He D., Kohorn B.D.;			
RT	"A cluster of five cell wall associated receptor kinase genes, WAK1-5			
RT	are expressed in specific organs of Arabidopsis."			
RL	Plant Mol. Biol. 39:1189-1196(1999).			
RN	[2]			
RE-	SEQUENCE FROM N.A.			
RA	Yamada K., Liu S.X., Sakano H., Pham P.K., Banh J., Chung M.K.,			
RA	Date J.M., Gibson H.A., Goldsmith A.D., Jiang F.X., Lee J.M.,			
RA	Quach H.T., Tang C., Toriumi M., Yu G., Bowser L., Carninci P.,			
RA	Chen H., Cheuk R., Hayashizaki Y., Ishida J., Jones T., Kamita A.,			
RA	Kallio-Neumann G., Kawal J., Kim C., Koeseema E., Lam B., Lin J.,			
RA	Meyers M.C., Miranda M., Narusaka M., Nguyen M., Palm C.J.,			
RA	Sakurai T., Satou M., Seki M., Shino P., Southgick A., Tracy S.E.,			
RA	Shinozaki K., Davis R.W., Ecker R.W., Theologis A.;			
RT	"Full length cDNA of gene F16F4.6 (GI:8920634)."			
RT	Submitted (JUN-2001) to the EMBL/GenBank/DBP databases.			
RL	-1- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.			
CC	EMBL; AJ008696; CA08794.1; -			
DR	EMBL; AY039917; AAK64021.1; -			
DR	InterPro: IPR000152; Asx_hydroxyl.			
DR	InterPro: IPR000561; EGF-1like.			
DR	InterPro: IPR001881; EGF-CA.			
DR	InterPro: IPR007719; Euk_kinase.			
DR	InterPro: IPR002290; Ser_thr_kinase.			
DR	InterPro: IPR004040; STY_kinase.			
DR	Pfam: PF00069; pkinase; 1.			
DR	ProDom: PD000001; Euk_pkinase; 1.			
DR	SMART; SM00179; EGF_CA; 1.			
DR	SMART; SM00001; EGF_1like; 1.			
DR	SMART; SM00221; STYKc; 1.			
DR	PROSITE: PS00010; ASX_HYDROXYL; UNKNOWN_1.			
DR	PROSITE: PS0186; EGF_2; UNKNOWN_1.			
DR	PROSITE: PS00187; EGF_CA; 1.			
DR	PROSITE: PS50011; PROTEIN_KINASE_DOM; 1.			
DR	PROSITE: PS00108; PROTEIN_KINASE_ST; 1.			
DR	ATP-binding; Calcium-binding; EGF-1like domain; Glycoprotein; kinase;			
KW	Repeat; Serine/threonine-protein kinase; Transferase.			
KW	SEQUENCE 735 AA; 81211 MW; AAD4IA28296093E6 CRO64;			
QY	8.3%; Score 80; DB 10; Length 735;			
QY	Best Local Similarity 24.2%; Pred. No. 8;			
QY	Matches 39; Conservative 27; Mismatches 49; Indels 46; Gaps			
DB	8 CSNVEFDSLHACICCO--LMCSSN-----TPTICOR-----VCMA-----SV 45			
DB	264 CRCHGEFGDNPRTISACQVNECTSTSIHHNCSDPKTRCNKVGCFYCQSGCRIDPT 3233			
QY	46 TNSVK-----GTNAIIWTCGLSLTISLAFLVFLTKRISSEPLDE-FKNTGSGLL-- 97			
DB	324 TMSCKRREFAFTTLLVTTIGF-LVLLIGVACIOCRKHLKDKTKRLEDFEONGGGMTO 3822			

QY 98 -----GMANID-----LEKRTG--DEILPRGLETV 123
 Db 383 RLSGAGPSNVQDKFTEDGMKATNGVAESRLDGGGQTV 423

RESULT 13

ID Q26489 PRELIMINARY; PRT: 1299 AA.

AC Q26489;
 DT 01-NOV-1996 (TREMBLrel. 01, Created)
 DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)
 DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)
 DE Endoprotease furin.
 GN FURIN.

OS Spodoptera frugiperda (Fall armyworm).
 OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
 OC Pterygota; Neoptera; Endopterygota; Lepidoptera; Glossata; Ditrysia;
 OC Noctuidae; Noctuidae; Amphipylinae; Spodoptera.
 OX NCBI_Taxid=7108;
 RN [1]

RP SEQUENCE FROM N.A.

RC TISSUE=SF;
 RA Clepik M., Klenk H.;
 RT "Cloning and functional characterization of FURIN from Spodoptera
 frugiperda (sf9) cells."
 RL Submitted (JAN-1996) to the EMBL/GenBank/DBJ databases.
 DR EMBL; 268888; CAA93116.1;
 DR HSP; 099405; IMPT.
 DR InterPro: IPR002174; Furin-1like.
 DR InterPro: IPR002039; Peptidase_S8.
 DR InterPro: IPR002884; P_domain.
 DR Pfam: PF01483; P_1.
 DR Pfam: PF00082; Peptidase_S8; 1.
 DR PRINTS: PR00723; SUBTILISIN.
 DR ProDom: PD000717; P_domain; 1.
 DR SMART: SM00261; FU; 10.
 DR PROSITE: PS00136; SUBTILASE_ASP; 1.
 DR PROSITE: PS00137; SUBTILASE_HIS; 1.
 DR PROSITE: PS00136; SUBTILASE_SER; 1.
 KW Protease.
 SQ SEQUENCE 1299 AA; 142020 MW; 4C3799C7BDC572AB CRC64;

Query Match 8.2%; Score 79.5; DB 5; Length 1299;
 Best Local Similarity 24.1%; Pred. No. 17;
 Matches 39; Conservative 26; Mismatches 48; Indels 49; Gaps 11;

QY 8 CSQNEFDSLHACIPQLKRS-----SNPPPLTCQRYCNAS-----VTSNKGTAAIL-W 57
 Db 1150 CSRPLRIDELNQCVCPC---CSEKGVNSTPTDC-CHCPENGECINSVAGKRRIAEW 1205
 QY 58 TGLGIS-----LIISLAV-----EYLMFLRKISSEPLKDEKNTGSLGMAN 101
 Db 1206 GALHTPSPADAPSAVAVTIACAAVGLFTVLVQLAISPREKTRTSVARG----- 1259
 QY 102 IDLEKSRGDEILPR-GLETVVECTCECISKRPVSDH 142
 Db 1260 --VEYSR-----LPRTVDFTV---LTSCDDECPVEYEH 1289

RESULT 14

ID Q8VFMO PRELIMINARY; PRT: 314 AA.

AC Q8VFMO;
 DT 01-MAR-2002 (TREMBLrel. 20, Created)
 DT 01-MAR-2002 (TREMBLrel. 20, Last sequence update)
 DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)
 DE Olfactory receptor MOR202-16.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Cranialata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathii; Muridae; Murinae; Mus.
 OX NCBI_Taxid=10090;
 RN [1]

RP SEQUENCE FROM N.A.

RA Zhang X., Firestein S.J.;
 RT "The olfactory receptor gene superfamily of the mouse."
 RL Nat. Neurosci. 0:0-0(2002).
 RN [2]

RP SEQUENCE FROM N.A.

RA Adams M.;
 RL Submitted (JAN-2002) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AY073405; AAL61068.1;
 DR InterPro: IPR000276; GPCR_Rhodopsn.
 DR Pfam: PF00001; 7tm.1; 1.
 DR PRINTS: PR00237; GPCR_RHODOPSN.
 DR PROSITE: PS00237; G_PROTEIN_RECPT_P1; UNKNOWN_1.
 DR PROSITE: PS00262; G_PROTEIN_RECPT_P1_2; 1.
 KW Receptor.

SQ SEQUENCE 314 AA; 34987 MW; DE5CDDF63E3B2PD8 CRC64;

Query Match 8.1%; Score 78.5; DB 11; Length 314;
 Best Local Similarity 30.4%; Pred. No. 4.4;
 Matches 31; Conservative 15; Mismatches 41; Indels 15; Gaps 6;

QY 8 CSQNEFDSLHACIP-CQLRCSSNT-----PPLTCQRYCNASVTSNKGTAAILMT 58
 Db 146 CYMCGTLOSHIHVALAFCLSPCNVNIHFPDIPPL-LDISGSDYTNEL--TVLIJGT 202
 QY 59 CLG-LSLIISLAVFLMF--LLRKISSEPLKDEKNTGSLGL 97
 Db 203 CDSILTLVILMTYLLIFALIRMSVLAQKATSTCSAHLI 244

RESULT 15

ID Q9H677 PRELIMINARY; PRT: 485 AA.

AC Q9H677;
 DT 01-MAR-2001 (TREMBLrel. 16, Created)
 DT 01-MAR-2001 (TREMBLrel. 16, Last sequence update)
 DT 01-MAR-2001 (TREMBLrel. 16, Last annotation update)
 DE CDNA: FLJ22531 f1s, clone hRC12890.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Cranialata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 OX NCBI_Taxid=9606;
 RN [1]

RP SEQUENCE FROM N.A.
 RA Kawabata A., Hiki J.T., Kobatake N., Inagaki H., Ikema Y., Okamoto S.,
 RA Ohtani R., Ota T., Suzuki Y., Odayashi M., Nishi T., Shibahara T.,
 RA Tanaka T., Nakamura Y., Isogai T., Sugano S.;
 RT "NEBO human cDNA sequencing project."
 RL Submitted (AUG-2000) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AK026184; BAB15387.1;
 SQ SEQUENCE 485 AA; 54051 MW; 4474E549ACD560C3 CRC64;

Query Match 8.1%; Score 78.5; DB 4; Length 485;
 Best Local Similarity 26.3%; Pred. No. 7.2;
 Matches 35; Conservative 17; Mismatches 48; Indels 33; Gaps 6;

QY 47 NSVKGTAAILMTCLGLSLISLAVFLMFLLRKISSEPLKDEKNTG-----GLLGM 99
 Db 185 NRISVSIFLYGPLGLPILS-----TWQPMPTFPKDTSSLYDWKKYHLICMI 232
 QY 100 ANIDLEKSRGDEILPRGLETVVECTCECISKRP-----YSDHCFPLPAME 150
 Db 233 PNLIDLNR---DIVLP-DVSYQVSSSEDSQTMDDGGOTLLFLFVDHSAFPVQONE 288
 QY 151 -EGATLVTTKTN 162
 Db 289 IMGVYTLTTHLN 301

Search completed: November 12, 2002, 17:00:18
 Job time : 59.0687 secs

PF 14-MAY-2001; 2001WO-US15567.
 XX
 PR 12-MAY-2000; 2000US-204039P.
 PR 27-JUN-2000; 2000US-214591P.
 PR 14-MAY-2001; 2001US-0214591.
 XX
 PA (AMGE-) AMGEN INC.
 XX
 PI Theill LE, Yu G;
 DR WPI: 2002-066686/09.
 XX
 PT Inhibiting activity of B cell maturation protein and/or transmembrane
 PT activator and intracellular cyclophilin ligand interactor, by
 PT administering a binding partner for APRIL, a tumor necrosis factor
 PT family ligand
 XX
 PS Disclosure: Fig 10A; 94pp; English.
 XX
 CC The invention relates to a method for inhibiting TACI (transmembrane
 CC activator and intracellular CAML interactor) and/or B cell maturation
 CC protein (BCMA) activity in a mammal. The method comprises administering
 CC a specific binding partner for APRIL (G70, a tumor necrosis factor-TNF
 CC family ligand), having the consensus sequence, but not the extracellular region
 CC of BCMA extracellular consensus sequence, but not the extracellular region
 CC of TACI or BCMA. The method is useful for inhibiting activity of TACI
 CC and/or BCMA in a mammal which is useful for treating B-cell or T-cell
 CC lymphoproliferative disorders, one or more solid tumours such as lung,
 CC gastrointestinal, pancreatic or prostate tumour, APRIL, BCMA and TACI
 CC antagonists are useful for treating inflammation and immune function
 CC diseases such as diarrhoea, psoriasis, allergies, pneumonia, atopic
 CC dermatitis, respiratory allergic disease (asthma, hypersensitivity lung
 CC disease), drug and insect sting allergy, inflammatory bowel disease
 CC (Crohn's disease, colitis), scleroderma, autoimmune disease (multiple
 CC sclerosis, rheumatoid arthritis, systemic lupus erythematosus), fungal,
 CC bacterial, protozoal and viral infections (HIV), atherosclerosis, cancer
 CC with leucocyte infiltration of the skin or organs. The present sequence
 CC is human BCMA protein.
 XX
 SQ Sequence 181 AA:
 XX
 QY Query Match 100.0%; Score 36; DB 23; Length 181;
 Best Local Similarity 100.0%; Pred. No. 5.6;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 EKSRTGD 7
 DB 102 EKSRTGD 108
 XX
 RESULT 2
 AAB08843
 ID AAB08843 standard; peptide; 184 AA.
 XX
 AC AAB08843;
 XX
 DT 02-JAN-2001 (first entry)
 DE Amino acid sequence of human.
 XX
 XX BCMA: necrosis factor- κ B activator; NF- κ B; gene expression; cancer;
 KM anti-cell death gene; apoptosis; viral infection; inflammatory response;
 KM rheumatoid arthritis; inflammatory bowel disease; septic shock.
 XX
 OS Homo sapiens.
 XX
 XX Key Location/Qualifiers
 FH 57..77
 FT Domain /note="putative transmembrane domain"
 XX
 PN WO200050633-A1.
 PD 31-AUG-2000.

XX
 XX 24-FEB-2000; 2000WO-US04925.
 XX
 PR 24-FEB-1999; 99US-0121485.
 XX
 PR (GEHO) GEN HOSPITAL CORP.
 XX
 PA Seed B, Ting A;
 XX
 PI WPI: 2000-558405/51.
 DR
 XX
 PT Identifying a modulator of gene expression for drug designing, by
 PT contacting a compound library with a cell expressing an anti-cell death
 PT gene and reporter gene, and determining alteration in reporter gene
 PT expression
 XX
 PS Claim 32; Fig 7A; 53pp; English.
 XX
 CC The present sequence represents a BCMA (not defined) polypeptide. BCMA
 CC is a necrosis factor (NF)- κ B activator. The method of the invention is
 CC used to identify compounds which modulate BCMA activity (and thus NF- κ B
 CC activity). The specification describes a method of identifying a
 CC polypeptide which increases gene expression from a promoter. The method
 CC involves contacting a library of with a cell which expresses a
 CC recombinant anti-cell death gene and a reporter gene operably linked to
 CC the promoter, and then determining whether the expression of the
 CC reporter gene is altered as a result of contact with library. The method
 CC is useful for identifying polypeptides which increase or decrease gene
 CC expression from a promoter. The BCMA polypeptide or nucleic acid are
 CC useful for preparing a pharmaceutical composition for treating cancer,
 CC apoptosis, viral infections, inflammatory response, such as rheumatoid
 CC arthritis, inflammatory bowel disease or septic shock. BCMA is useful for
 CC identifying compounds that modulate NF- κ B expression and thus for drug
 CC designing.
 XX
 SQ Sequence 184 AA:
 XX
 QY Query Match 100.0%; Score 36; DB 21; Length 184;
 Best Local Similarity 100.0%; Pred. No. 5.7;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 EKSRTGD 7
 DB 105 EKSRTGD 111
 XX
 RESULT 3
 AAY94001
 ID AAY94001 standard; Protein; 184 AA.
 XX
 AC AAY94001;
 XX
 DT 20-OCT-2000 (first entry)
 DE A human BCMA protein, a B cell protein related to TACI.
 XX
 XX Human; BR43x2; TACI receptor; extracellular domain; BCMA; B cell protein;
 KM transmembrane activator and CAML-interactor; tumour necrosis factor; TNF;
 KM zntf4 activity; antibody production; autoimmune disease; amyloidosis;
 KM systemic lupus erythematosus; myasthenia gravis; multiple sclerosis;
 KM rheumatoid arthritis; asthma; bronchitis; emphysema; pyelonephritis;
 KM end stage renal failure; glomerulonephritis; vasculitis; nephritis;
 KM renal neoplasms; multiple myeloma; lymphoma; light chain neuropathy;
 KM immune response; immunosuppression; graft rejection; joint pain;
 KM graft versus host disease; inflammation; swelling; anaemia; septic shock;
 KM insulin dependent diabetes mellitus; Crohn's disease; hypertension;
 KM renal artery stenosis; occlusion; cholesterol; renal emboli.
 XX
 OS Homo sapiens.
 XX
 XX WO200040716-A2.
 PN
 PD 13-JUL-2000.

XX 07-JAN-2000; 2000MO-US00396.
 PF
 XX
 XX 07-JAN-1999; 99US-0226533.
 PR
 XX
 XX (ZYMO) ZYMOGENETICS INC.
 PA
 XX
 XX Gross JA, Xu W, Madden K, Yee DP.
 PI
 XX WPI: 2000-452538/39.
 DR
 XX N-PSDB: AAA58559.
 DR
 XX
 PT Inhibiting ztnf4 activity in a mammal, to treat autoimmune diseases,
 PT renal disease, graft versus host disease, and inflammation, comprises
 PT administering a BR43x2, TACI or BCMA extracellular domain polypeptide -
 PT
 XX
 PS Disclosure: Page 152; 175pp; English.
 PS
 XX The present sequence represents a human BCMA protein, a B cell protein
 CC related to transmembrane activator and CAML-interactor (TACI) receptor.
 CC TACI is a tumour necrosis factor (TNF) receptor. The extracellular
 CC domains of BR43x2 (an isoform of TACI), TACI or BCMA (a related B cell
 CC protein) receptor contain a cysteine rich domain, and are used for
 CC inhibiting ztnf4 activity. ztnf4 is a TNF ligand. They may also be used
 CC for inhibiting BR43x2, TACI or BCMA receptor-ligand engagement associated
 CC with activated or resting B lymphocytes, effector T-cells, or with
 CC antibody production. The antibody production is associated with an
 CC autoimmune disease selected from systemic lupus erythematosus, myasthenia
 CC gravis, multiple sclerosis and rheumatoid arthritis. The ztnf4 activity
 CC and BR43x2, TACI or BCMA receptor-ligand engagement is associated with
 CC asthma, bronchitis, emphysema, end stage renal failure,
 CC glomerulonephritis, vasculitis, nephritis, pyelonephritis, renal
 CC neoplasms, multiple myelomas, lymphomas, light chain neuropathy,
 CC amyloidosis, moderating immune response, immunosuppression, graft
 CC rejection, graft versus host disease, inflammation, insulin dependent
 CC diabetes mellitus, Crohn's disease, joint pain, swelling, anaemia, or
 CC septic shock. BR43x2, TACI, and BCMA polypeptides, fusions, antibodies,
 CC agonists or antagonists can be used to treat hypertension, renal artery
 CC stenosis, or occlusion, and cholesterol or renal emboli.
 CC
 XX
 SO Sequence 184 AA:
 SO
 Query Match 100.0%; Score 36; DB 21; Length 184;
 Best Local Similarity 100.0%; Pred. No. 5.7;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 OY 1 EKSRTGD 7
 DB 105 EKSRTGD 111
 DB
 RESULT 4
 AAE09241
 ID AAE09241 standard; Protein: 184 AA.
 XX
 AC AAE09241;
 XX
 DT 19-NOV-2001 (first entry)
 XX
 DE Human BCMA protein.
 XX
 KW Human: TNF, tumour necrosis factor; TALL-1; APRIL; TNF receptor;
 KW TNFR; TACI; BCMA; therapy: cancer; leukaemia; myeloma; lymphoma;
 KW autoimmune disease; rheumatoid arthritis; multiple sclerosis;
 KW psoriasis.
 KW
 OS Homo sapiens.
 XX
 XX WO200160397-A1.
 PN
 XX 23-AUG-2001.
 PD
 XX 28-NOV-2000; 2000MO-US32378.
 PF

XX 16-FEB-2000; 2000US-0182938.
 PR
 PR 22-AUG-2000; 2000US-0226986.
 PR
 XX (GETH) GENENTECH INC.
 PA
 XX
 XX Ashkenazi AJ, Dodge KH, Grewal I, Kim KJ, Maisters SA, Pitti RM;
 PI Yan M;
 PI
 XX WPI: 2001-541628/60.
 DR
 XX N-PSDB: AAD15902.
 DR
 XX
 PT Inhibiting or neutralizing TALL-1 or APRIL polypeptide biological
 PT activity, for treating autoimmune disorders and cancer, comprises
 PT exposing the cells to TALL-1 or APRIL polypeptide agonists or
 PT antagonists -
 PT
 XX
 PS Example 2; Fig 2; 160pp; English.
 PS
 XX The invention relates to methods of using one or more agonists or
 CC antagonists to modulate the activity of the members of TNF (tumour
 CC necrosis factor) especially TALL-1, APRIL, and TNF receptor (TNFR)
 CC e.g. TACI or BCMA. The method is useful for treating pathological
 CC conditions or diseases associated with increased TALL-1 and APRIL
 CC expression or activity. TALL-1 and APRIL antagonists are used to
 CC block the interaction between APRIL and TALL-1 with TACI or BCMA.
 CC They are useful for treating a mammal suffering from cancer such
 CC as leukaemia, lymphoma, myeloma, cancers of lung and colon and
 CC autoimmune diseases e.g. rheumatoid arthritis, multiple sclerosis,
 CC psoriasis and lupus erythematosus. The present sequence is human
 CC BCMA protein.
 CC
 XX
 SO Sequence 184 AA:
 SO
 Query Match 100.0%; Score 36; DB 22; Length 184;
 Best Local Similarity 100.0%; Pred. No. 5.7;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 OY 1 EKSRTGD 7
 DB 105 EKSRTGD 111
 DB
 RESULT 5
 AAE00506
 ID AAE00506 standard; Protein: 184 AA.
 XX
 AC AAE00506;
 XX
 DT 31-JUL-2001 (first entry)
 XX
 DE Human B cell maturation protein (BCMA).
 XX
 KW Human: A Proliferation Inducing Ligand Receptor; APRIL-R; cytostatic;
 KW gene therapy; cancer; nephrotropic; renal disorder; autoimmune disease;
 KW carcinoma; lung; colon; breast; prostate; Grave's disease; hypertension;
 KW systemic lupus erythematosus; SLE; inflammation; cardiovascular disease;
 KW B-cell lympho-proliferative disorder; BCM; immunosuppressive disease;
 KW organ transplantation; HIV; human immunodeficiency virus; TNF;
 KW tumour necrosis factor; BCMA; B cell maturation protein.
 KW
 OS Homo sapiens.
 XX
 XX WO200124811-A1.
 PN
 XX 12-APR-2001.
 PD
 XX 05-OCT-2000; 2000MO-US27579.
 PF
 XX 06-OCT-1999; 99US-0157933.
 PR 11-FEB-2000; 2000US-0181807.
 PR 30-JUN-2000; 2000US-0215688.
 PR
 XX

Query	Match	Similarity	Score	DB	Length	184:
Best Local	Similarity	100.08;	Pred. NO. 5.7;			
Matches	7;	Conservative	0;	Mismatches	0;	Indels
Gaps						
1 EKSRTCD 7						
105 EKSRTGD 111						
RESULT 6						
AAB60698						
ID	AAB60698	standard;	Protein: 184	AA.		
XX	AAB60698;					
XX						
DT	22-MAY-2001	(first entry)				
DE	Human BAFF receptor (BAFF-R).					
XX						
KW	Human BAFF-R; BAFF receptor; TNF family; immunoregulatory agent;					
KW	immune-related disorder; B-cell growth inhibitor; BCMA;					
KW	autoimmune disorder; B-cell lymphoproliferative disorder; hyperlenson;					
KW	renal disorder; immunosuppressive disorder; HIV infection;					
KW	organ transplantation; antinflammatory; systemic lupus erythematosus;					
KW	autoimmune haemolytic anaemia; Grave's disease; multiple myeloma;					
KW	B-cell carcinoma; leukemia; rapidly progressive glomerulonephritis;					
XX	lymphoma; gene therapy; cancer; tumour.					
XX						
OS	Homo sapiens.					
PN	MO200112812-A2.					
PD	22-FEB-2001.					
XX						
XX	16-AUG-2000; 2000WC-US22507.					
XX						

PR	17-AUG-1999:	99US-0149378.	
PR	11-FEB-2000:	2000US-0181684.	
PR	18-FEB-2000:	2000US-0183536.	
XX			
PA	(BIOJ) BIOGEN INC.		
PA	(APOT-) APOTEC R & D SA.		
XX			
PI	McKAY F., Browning J., Ambrose C., Tschopp J., Schneider P;		
PI	Thompson J;		
XX			
DR	WPI: 2001-202866/20.		
XX	N-PSDB: AAF59998.		
PT	Inhibiting dendritic cell-induced B-cell growth, maturation and B-cell		
PT	lympho-proliferative disorder by administering BAF-R-receptor		
PT	polypeptide, chimeric molecule comprising receptor or anti-BAF-R		
PT	antibody homolog -		
XX			
PS	Claim 20; Fig 1; 59pp: English.		
XX			
CC	The invention relates to the use of a BAF-R receptor (BAF-R, also known		
CC	as BCMA) protein, or a BAF-R fusion protein as an agent for the		
CC	treatment of a variety of immune-related disorders. BAF-R is a member of		
CC	the TNF (tumour necrosis factor) family, acting as an immunoregulatory		
CC	agent, and also plays a role in the development of hypertension and		
CC	related disorders. BAF-R, fusion proteins containing it, and BAF-R-		
CC	specific antibodies can be used for inhibiting B-cell growth, dendritic		
CC	cell-induced B-cell growth and maturation, and immunoglobulin production,		
CC	and in the treatment of autoimmune disorders, B-cell lymphoproliferative		
CC	disorders, hypertension and renal disorders. The BAF-R proteins may also		
CC	be used in the treatment of immunosuppressive disorders and HIV		
CC	infection, and in patients undergoing organ transplantation. The BAF-R		
CC	proteins or BAF-R-specific antibodies may be used for treating,		
CC	suppressing or altering an immune response involving a signalling pathway		
CC	between BAF-R and BAF-R, thereby inhibiting inflammation. Since BAF-R		
CC	inhibits B-cell growth and maturation it is useful for treating diseases		
CC	such as systemic lupus erythematosus, autoimmune haemolytic anaemia,		
CC	grave's disease, multiple myeloma, B-cell carcinomas, leukemias, rapidly		
CC	progressive glomerulonephritis, and lymphomas. Nucleic acids encoding		
CC	human BAF-R may be used in gene therapy to treat tumours, lymphomas,		
CC	autoimmune disorders and inherited B-cell-associated disorders. The		
CC	present sequence represents human BAF-R.		
XX			
SC	Sequence 184 AA:		
QY	1 EKSRTGD 7		
QY	105 EKSRTGD 111		
QY	100.0%; Score 36; DB 22; Length 184;		
QY	Best Local Similarity 100.0%; Pred. No. 5.7;		
QY	Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0.		
XX			
RESULT 7			
ID	AAV71979		
XX	AAV71979 standard; protein: 184 AA.		
XX	AAV71979:		
XX	28-MAR-2001 (first entry)		
XX			
DE	Human B cell maturation factor (BCMA) protein.		
KW	Human; Tumour Necrosis Factor; TNF; leucocypressant; TALL-1;		
KW	Tumour necrosis factor and Apol-related leucocyte expressed ligand 1;		
KW	therapy; autoimmune disorder; Rheumatoid arthritis; multiple sclerosis;		
KW	systemic lupus erythematosus; SLE; insulin dependent diabetes mellitus;		
KW	thrombocytopenia purpura; acute rheumatic fever; Goodpasture's syndrome;		
KW	haemolytic anaemia; Grave's disease; myasthenia gravis; chromosome 16;		
KW	post-streptococcal glomerulonephritis; polyarteritis nodosa; BCMA;		
KW	B cell maturation factor; pemphigus vulgaris; B-lymphocyte proliferation.		

OS Homo sapiens.
 XX Key Location/Qualifiers
 FT Domain 1..62 /label= Extracellular_domain
 XX
 XX MO200068378-A1.
 XX
 XX 16-NOV-2000.
 XX
 XX 05-MAY-2000; 2000MO-US12266.
 XX
 XX 06-MAY-1999; 99US-0132892.
 XX
 XX 01-MAY-2000; 2000US-0201012.
 XX
 XX (NAJE-) NAT JEWISH MEDICAL & RES. CENT.
 XX
 XX Shu HS.
 XX
 XX WPI: 2001-016094/02.
 XX
 XX N-PSDB; AAD02125.
 XX
 XX Isolated TALL-1 protein is used to identify compounds that regulate B
 PT lymphocyte proliferation, used to treat B lymphocyte associated
 PT autoimmune disorders -
 XX
 XX Claim 37; Page 104-105; 112pp; English.
 XX
 XX The present invention relates to Tumour necrosis factor (TNF) and
 CC Apol-related Leucocyte expressed ligand 1 (TALL-1) nucleic acid
 CC molecules, proteins (including homologues), and their antibodies. The
 CC invention in particular relates to methods for regulating the
 CC interaction between TALL-1 and TALL-1 receptors (BCMA referred as B cell
 CC maturation factor) to regulate monocyte, macrophage and B lymphocyte
 CC mediated immune responses. TALL-1 protein is useful for identifying
 CC compounds that regulate B lymphocyte proliferation. It is also useful for
 CC treating B lymphocyte associated autoimmune disorders like Rheumatoid
 CC arthritis, systemic lupus erythematosus (SLE), insulin dependent diabetes
 CC mellitus, multiple sclerosis, myasthenia gravis, Grave's disease,
 CC autoimmune haemolytic anaemia, autoimmune thrombocytopenia purpura,
 CC Goodpasture's syndrome, pemphigus vulgaris, acute rheumatic fever,
 CC post-streptococcal glomerulonephritis, or polyarteritis nodosa.
 CC The TALL-1 protein and its corresponding nucleic acid sequence are also
 CC useful in diagnostic assays.
 CC The present sequence is a human B cell maturation factor (BCMA)
 CC protein. It is the receptor for TALL-1 protein. BCMA gene is
 CC located on chromosome 16. In human tissues, BCMA is expressed by
 CC spleen and lymph nodes but not by brain, muscle, heart, lung, kidney,
 CC pancreas, testis and placenta. BCMA mRNA is absent in the pro-B
 CC lymphocyte stage but its expression increases with B lymphocyte
 CC maturation.
 CC
 XX Sequence 184 AA:
 XX
 QY Query Match 100.0%; Score 36; DB 22; Length 184;
 DB Best Local Similarity 100.0%; Pred. No. 5.7;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 EKSRTGD 7
 DB 105 EKSRTGD 111
 DB
 RESULT 8
 ABB81487
 ID ABB81487 standard; Protein: 184 AA.
 XX
 XX ABB81487;
 XX
 XX 02-SEP-2002 (first entry)
 XX
 XX Human BCMA receptor related protein SEQ ID NO:7.
 XX
 XX

KM Human; Znftr12; tumour necrosis factor receptor; cytosolic;
 KM immunosuppressive; dermatological; antiinflammatory; antidiabetic;
 KM neutroprotective; antirheumatic; antiarthritic; antiasthmatic;
 KM nephrotropic; hypotensive; gene therapy; B lymphocyte; tumour;
 KM autoimmune disorder; systemic lupus erythematosus; myasthenia gravis;
 KM multiple sclerosis; insulin dependent diabetes mellitus; asthma;
 KM rheumatoid arthritis; bronchitis; emphysema; renal disease; lymphoma;
 KM glomerulonephritis; vasculitis; chronic lymphoid leukaemia; nephritis;
 KM pyelonephritis; renal neoplasm; multiple myeloma; amyloidosis;
 KM light chain neuropathy; hypertension; large vessel disease;
 KM graft-versus host disease; graft rejection; Crohn's disease.
 XX
 OS Homo sapiens.
 XX
 XX MO200238766-A2.
 XX
 XX 16-MAY-2002.
 XX
 XX 05-NOV-2001; 2001MO-US47018.
 XX
 XX 07-NOV-2000; 2000US-246449P.
 XX
 XX 20-DEC-2000; 2000US-257131P.
 XX
 XX 28-JUN-2001; 2001US-301715P.
 XX
 XX 29-AUG-2001; 2001US-315565P.
 XX
 XX (ZYMO) ZYMOGENETICS INC.
 XX
 XX Gross JA, Xu W, Henne RM, Grant FJ;
 XX
 XX WPI: 2002-508212/54.
 XX
 XX Novel isolated human tumor necrosis factor receptor polypeptide, termed
 PT Znftr 12, useful for treating autoimmune disorders, emphysema, end
 PT stage renal failure or renal disease and lymphoma
 XX
 XX Disclosure: Page 135-136; 154pp; English.
 XX
 XX The present invention describes a human tumour necrosis factor receptor
 CC designated Znftr12 (1). (1) has cytosolic, immunosuppressive,
 CC dermatological, antiinflammatory, neutroprotective, antidiabetic,
 CC antirheumatic, antiarthritic, antiasthmatic, nephrotropic and hypotensive
 CC activities, and can be used in gene therapy. (1) can be used for
 CC inhibiting, in a mammal, the activity of a ligand that binds Znftr12
 CC (e.g. ZTNF4), for treating disorders and diseases associated with B
 CC lymphocytes, activated B lymphocytes or resting B lymphocytes, and for
 CC inhibiting the proliferation of tumour cells. (1) is useful for treating
 CC autoimmune disorders such as systemic lupus erythematosus, myasthenia
 CC gravis, multiple sclerosis, insulin dependent diabetes mellitus, asthma,
 CC rheumatoid arthritis, bronchitis, emphysema and end stage renal failure
 CC or renal disease such as glomerulonephritis, vasculitis, chronic lymphoid
 CC leukaemia, nephritis, and pyelonephritis, and for treating renal
 CC neoplasms, multiple myelomas, lymphomas, light chain neuropathy, or
 CC amyloidosis, hypertension, large vessel diseases, graft-versus host
 CC disease, graft rejection and Crohn's disease. (1) is useful for
 CC modulating the immune system, for regulating B cell responses and
 CC development, for modulating development of other cells, antibody
 CC production and cytokine production, and for modulating T and B cell
 CC communication. The present sequence represents a protein which is
 CC given in the exemplification of the present invention.
 CC
 XX Sequence 184 AA:
 XX
 QY Query Match 100.0%; Score 36; DB 23; Length 184;
 DB Best Local Similarity 100.0%; Pred. No. 5.7;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 EKSRTGD 7
 DB 105 EKSRTGD 111
 DB
 RESULT 9
 AAY00041

```

ID  AA00041 standard; Protein; 521 AA.
XX
AC  AA00041;
XX
DT  20-APR-1999 (first entry)
XX
DE  Enterococcus faecalis antigenic polypeptide fragment EF017.
XX
KM  Enterococcus faecalis; infection; vaccine; immune response; diagnosis;
XX  detection; attenuation; antigenic.
OS  Enterococcus faecalis.
XX
PN  W09850554-A2.
XX
PD  12-NOV-1998.
XX
PF  04-MAY-1998; 98WO-US08959.
XX
PR  14-NOV-1997; 97US-0066009.
PR  06-MAY-1997; 97US-0044031.
PR  16-MAY-1997; 97US-0046555.
XX
PA  (HUMA-) HUMAN GENOME SCI INC.
XX
PI  Bailey C, Choi GH, Hromocky] A, Kunsch CA;
XX  WPI: 1999-070095/06.
DR  N-PSDB; AAX20031.
XX
PT  New isolated Enterococcus faecalis polynucleotides - used to develop
PT  products for the detection of Enterococcus and for use in vaccines
PT  for prevention or attenuation of Enterococcus infection
XX
PS  Claim 9; Page 96; 301pp; English.
XX
CC  The present sequence represents an antigenic polypeptide fragment
CC  isolated from Enterococcus faecalis. The present invention describes
CC  genes, proteins and antigenic polypeptides isolated from E. faecalis.
CC  The proteins can be used in vaccines for preventing or attenuating an
CC  infection caused by a member of the Enterococcus genus in an animal.
CC  They can also be used for detecting Enterococcus antibodies in a sample.
CC  The nucleotide sequences can be used for detecting Enterococcus nucleic
CC  acids. Products from the present invention can also be used for
CC  screening compounds to identify agonists and antagonists of E. faecalis
CC  protein activity.
CC
XX  Sequence 521 AA;
XX
Query Match 88.9%; Score 32; DB 20; Length 521;
Best Local Similarity 85.7%; Pred. No. 1,1e+02;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
OY 1 EKSRTGD 7
DB 405 EKSRTGD 411
XX
RESULT 10
ABP43260
ID ABP43260 standard; Protein; 521 AA.
XX
AC ABP43260;
XX
DT 05-AUG-2002 (first entry)
XX
DE E faecalis EF017 antigenic fragment.
XX
KM Enterococcus; vaccine; gastrointestinal disease; diagnosis; antibiotic.
XX  Enterococcus faecalis.
XX
OS Enterococcus faecalis.
XX
PN US2002045737-A1.

```

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XX
PD 18-APR-2002.
XX
XX 04-MAY-1998; 98US-0071035.
XX
PF 04-MAY-1998; 98US-0071035.
XX
PR 04-MAY-1998; 98US-0071035.
XX
PA (HUMA-) HUMAN GENOME SCI INC.
XX
PI Choi GH, Bailey C, Hromocky] A, Kunsch CA;
XX  WPI: 2002-425450/45.
DR 2002-425450/45.
DR N-PSDB; AEN98016.
XX
PT New genes and polypeptides from Enterococcus faecalis, useful as
PT vaccines for preventing, treating or attenuating an infection caused by
PT a member of the Enterococcus genus in an animal, particularly E.
PT faecalis -
XX
XX Claim 9; Page 48; 255pp; English.
XX
PS The present invention provides the protein and coding sequences of a
XX number of polypeptides from Enterococcus faecalis. The proteins can be
XX used as vaccines for preventing or attenuating an infection caused by a
XX member of the Enterococcus genus in an animal, particularly E. faecalis.
XX The polynucleotide is also useful for preventing or treating E. faecalis
XX infection. The present sequence is a protein of the invention.
XX
XX Sequence 521 AA;
XX
Query Match 88.9%; Score 32; DB 23; Length 521;
Best Local Similarity 85.7%; Pred. No. 1,1e+02;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
OY 1 EKSRTGD 7
DB 405 EKSRTGD 411
XX
RESULT 11
AA00040
ID AA00040 standard; Protein; 542 AA.
XX
AC AA00040;
XX
DT 20-APR-1999 (first entry)
XX
DE Enterococcus faecalis protein EF017.
XX
XX
KM Enterococcus faecalis; infection; vaccine; immune response; diagnosis;
KM  detection; attenuation; antigenic.
XX
OS Enterococcus faecalis.
XX
PN W09850554-A2.
XX
PD 12-NOV-1998.
XX
PF 04-MAY-1998; 98WO-US08959.
XX
PR 14-NOV-1997; 97US-0066009.
PR 06-MAY-1997; 97US-0044031.
PR 16-MAY-1997; 97US-0046555.
XX
PA (HUMA-) HUMAN GENOME SCI INC.
XX
PI Bailey C, Choi GH, Hromocky] A, Kunsch CA;
XX  WPI: 1999-070095/06.
DR N-PSDB; AAX20030.
XX
PT New isolated Enterococcus faecalis polynucleotides - used to develop
PT products for the detection of Enterococcus and for use in vaccines

```

```
PT for prevention or attenuation of Enterococcus infection
XX
PS Claim 9; Page 95-96; 301pp; English.
XX
CC The present sequence represents a protein isolated from
CC Enterococcus faecalis. The present invention describes genes, proteins
CC and antigenic polypeptides isolated from E. faecalis. The proteins can
CC be used in vaccines for preventing or attenuating an infection caused
CC by a member of the Enterococcus genus in an animal. They can also be
CC used for detecting Enterococcus antibodies in a sample. The nucleotide
CC sequences can be used for detecting Enterococcus nucleic acids.
CC Products from the present invention can also be used for screening
CC compounds to identify agonists and antagonists of E. faecalis protein
CC activity.
XX
XX
S0 Sequence 542 AA;
Query Match 88.9%; Score 32; DB 20; Length 542;
Best Local Similarity 85.7%; Pred. No. 1.2e+02;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY 1 EKSRTGD 7
|111111
Db 426 EKSRSQD 432
RESULT 12
ABP43259 standard; Protein: 542 AA.
XX
XX ABP43259;
XX
XX 05-AUG-2002 (first entry)
XX
XX E faecalis EF017 protein.
XX
XX Enterococcus; vaccine; gastrointestinal disease; diagnosis; antibiotic.
XX
XX Enterococcus faecalis.
XX
XX US2002045737-A1.
XX
XX 18-APR-2002.
XX
XX 04-MAY-1998; 98US-0071035.
XX
XX 04-MAY-1998; 98US-0071035.
XX
XX (HUMA-) HUMAN GENOME SCI INC.
XX
XX Choi GH, Bailey C, Bromocky A, Kunsch CA;
XX
XX WPI: 2002-425450/45.
XX
XX N-PSDB; ABN98015.
XX
XX New genes and polypeptides from Enterococcus faecalis, useful as
XX vaccines for preventing, treating or attenuating an infection caused by
XX a member of the Enterococcus genus in an animal, particularly E.
XX faecalis
XX
XX Claim 9; Page 47; 255pp; English.
XX
XX The present invention provides the protein and coding sequences of a
XX number of polypeptides from Enterococcus faecalis. The proteins can be
XX used as vaccines for preventing or attenuating an infection caused by a
XX member of the Enterococcus genus in an animal, particularly E. faecalis.
XX The polynucleotide is also useful for preventing or treating E. faecalis
XX infection. The present sequence is a protein of the invention.
XX
S0 Sequence 542 AA;
Query Match 88.9%; Score 32; DB 23; Length 542;
Best Local Similarity 85.7%; Pred. No. 1.2e+02;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY 1 EKSRTGD 7
|111111
Db 426 EKSRSQD 432
RESULT 13
ABG29063 standard; Protein: 969 AA.
XX
XX ID ABG29063 standard; Protein: 969 AA.
XX
XX AC ABG29063;
XX
XX 18-FEB-2002 (first entry)
XX
XX Novel human diagnostic protein #29054.
XX
XX Human; chromosome mapping; gene mapping; gene therapy; forensic;
XX food supplement; medical imaging; diagnostic; genetic disorder.
XX
XX Homo sapiens.
XX
XX WO200175067-A2.
XX
XX 11-OCT-2001.
XX
XX 30-MAR-2001; 2001WO-US08631.
XX
XX 31-MAR-2000; 2000US-0540217.
XX
XX 23-AUG-2000; 2000US-0649167.
XX
XX (HYSE-) HYSEO INC.
XX
XX Dirmancic RT, Liu C, Tang YF;
XX
XX WPI: 2001-639362/73.
XX
XX N-PSDB; AAS933250.
XX
XX New isolated polynucleotide and encoded polypeptides, useful in
XX diagnostics, forensics, gene mapping, identification of mutations
XX responsible for genetic disorders or other traits and to assess
XX biodiversity
XX
XX Claim 20; SEQ ID No 59422; 103pp; English.
XX
XX The invention relates to isolated polynucleotide (I) and
XX polypeptide (II) sequences. (I) is useful as hybridisation probes,
XX polymerase chain reaction (PCR) primers, oligomers, and for chromosome
XX and gene mapping, and in recombinant production of (II). The
XX polynucleotides are also used in diagnostics as expressed sequence tags
XX for identifying expressed genes. (I) is useful in gene therapy techniques
XX to restore normal activity of (II) or to treat disease states involving
XX (II). (II) is useful for generating antibodies against it, detecting or
XX quantitating a polypeptide in tissue, as molecular weight markers and as
XX a food supplement. (II) and its binding partners are useful in medical
XX imaging of sites expressing (II). (I) and (II) are useful for treating
XX disorders involving aberrant protein expression or biological activity.
XX The polypeptide and polynucleotide sequences have applications in
XX diagnostics, forensics, gene mapping, identification of mutations
XX and to produce other types of data and products dependent on DNA and
XX amino acid sequences. ABG00010-ABG30377 represent novel human
XX diagnostic amino acid sequences of the invention.
XX Note: The sequence data for this patent did not appear in the printed
XX specification, but was obtained in electronic format directly from WIPO
XX at ftp.wipo.int/pub/published_pcl_sequences.
XX
S0 Sequence 969 AA;
Query Match 88.9%; Score 32; DB 22; Length 969;
Best Local Similarity 85.7%; Pred. No. 2.1e+02;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
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OY 1 EKSRGTD 7
DB 463 KKSRTGD 469

RESULT 14
ABR62925
ID ABR62925 standard; Protein; 1118 AA.
XX
AC ABR62925;
XX
DT 26-MAR-2002 (first entry)
XX
DE Drosophila melanogaster polypeptide SEQ ID NO 15567.
XX
KW Drosophila; developmental biology; cell signalling; insecticide;
XX pharmaceutical.
XX
OS Drosophila melanogaster.
XX
PN MO200171042-A2.
XX
PD 27-SEP-2001.
XX
PE 23-MAR-2001; 2001MO-US09231.
XX
PR 23-MAR-2000; 2000US-191637P.
PR 11-JUL-2000; 2000US-0614150.
XX
PA (PEKE) PE CORP NY.
XX
PI Venter JC, Adams M, LI PWD, Myers EW;
XX WPI: 2001-656860/75.
DR N-PSDB: ABL07028.
XX
PT New isolated nucleic acid detection reagent for detecting 1000 or more
PT genes from Drosophila and for elucidating cell signalling and cell-cell
PT interactions -
XX
PS Disclosure; SEQ ID NO 15567; 21pp + Sequence Listing; English.
XX
CC The invention relates to an isolated nucleic acid detection reagent
CC capable of detecting 1000 or more genes from Drosophila. The invention is
CC useful in developmental biology and in elucidating cell signalling and
CC cell-cell interactions in higher eukaryotes for the development of
CC insecticides, therapeutics and pharmaceutical drugs. The invention
CC discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA
CC sequences (ABL01840-ABL16175) and the encoded proteins
CC (ABR57737-ABR72072).
CC The sequence data for this patent did not form part of the printed
CC specification, but was obtained in electronic format directly from WIPO
CC at ftp.wipo.int/pub/published_pcc_sequences.
XX
SO Sequence 1118 AA;

Query Match 88.9%; Score 32; DB 22; Length 1118;
Best Local Similarity 85.7%; Pred. No. 2.4e+02;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 EKSRGTD 7
DB 986 EKDRGTD 992

RESULT 15
AAG21219
ID AAG21219 standard; Protein; 281 AA.
XX
AC AAG21219;
XX
DT 17-OCT-2000 (first entry)
XX

DE Arabidopsis thaliana protein fragment SEQ ID NO: 23696.
XX
KW Protein identification; signal transduction pathway; metabolic pathway;
KW hybridisation assay; genetic mapping; gene expression control; promoter;
KW termination sequence.
XX
OS Arabidopsis thaliana.
XX
PN EP1033405-A2.
XX
PD 06-SEP-2000.
XX
PE 25-FEB-2000; 2000EP-0301439.
XX
PR 25-FEB-1999; 99US-0121825.
PR 05-MAR-1999; 99US-0123180.
PR 09-MAR-1999; 99US-0123548.
PR 23-MAR-1999; 99US-0125788.
PR 25-MAR-1999; 99US-0126264.
PR 29-MAR-1999; 99US-0126785.
PR 01-APR-1999; 99US-0127462.
PR 06-APR-1999; 99US-0128234.
PR 08-APR-1999; 99US-0128714.
PR 16-APR-1999; 99US-0129845.
PR 19-APR-1999; 99US-0130077.
PR 21-APR-1999; 99US-0130449.
PR 23-APR-1999; 99US-0130510.
PR 28-APR-1999; 99US-0130891.
PR 30-APR-1999; 99US-0131449.
PR 30-APR-1999; 99US-0132048.
PR 04-MAY-1999; 99US-0132407.
PR 04-MAY-1999; 99US-0132484.
PR 05-MAY-1999; 99US-0132485.
PR 06-MAY-1999; 99US-0132486.
PR 06-MAY-1999; 99US-0132487.
PR 07-MAY-1999; 99US-0132863.
PR 11-MAY-1999; 99US-0134256.
PR 14-MAY-1999; 99US-0134218.
PR 14-MAY-1999; 99US-0134219.
PR 14-MAY-1999; 99US-0134221.
PR 14-MAY-1999; 99US-0134370.
PR 18-MAY-1999; 99US-0134768.
PR 19-MAY-1999; 99US-0134941.
PR 20-MAY-1999; 99US-0135124.
PR 21-MAY-1999; 99US-0135353.
PR 24-MAY-1999; 99US-0135629.
PR 25-MAY-1999; 99US-0136021.
PR 27-MAY-1999; 99US-0136392.
PR 28-MAY-1999; 99US-0136782.
PR 01-JUN-1999; 99US-0137222.
PR 03-JUN-1999; 99US-0137528.
PR 04-JUN-1999; 99US-0137502.
PR 07-JUN-1999; 99US-0137724.
PR 08-JUN-1999; 99US-0138094.
PR 10-JUN-1999; 99US-0138540.
PR 10-JUN-1999; 99US-0138847.
PR 14-JUN-1999; 99US-0139119.
PR 16-JUN-1999; 99US-0139452.
PR 16-JUN-1999; 99US-0139453.
PR 17-JUN-1999; 99US-0139492.
PR 18-JUN-1999; 99US-0139454.
PR 18-JUN-1999; 99US-0139455.
PR 18-JUN-1999; 99US-0139456.
PR 18-JUN-1999; 99US-0139457.
PR 18-JUN-1999; 99US-0139458.
PR 18-JUN-1999; 99US-0139459.
PR 18-JUN-1999; 99US-0139460.
PR 18-JUN-1999; 99US-0139461.
PR 18-JUN-1999; 99US-0139462.
PR 18-JUN-1999; 99US-0139463.
PR 18-JUN-1999; 99US-0139750.
PR 18-JUN-1999; 99US-0139763.
PR 21-JUN-1999; 99US-0139817.

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OM protein - protein search, using sw model

Run on: November 12, 2002, 16:57:01 : Search time 0.961373 Seconds
(without alignments)
214.236 Million cell updates/sec

Title: US-09-848-271-2_COPY_105_111

Perfect score: 36

Sequence: 1 EKSRTGD 7

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 262574 seqs, 29422922 residues

Total number of hits satisfying chosen parameters: 262574

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued_Patents_AA:*

1: /cgn2_6/ptodata1/1/aa/5A.COMB.pep:*
2: /cgn2_6/ptodata1/1/aa/5B.COMB.pep:*
3: /cgn2_6/ptodata1/1/aa/6A.COMB.pep:*
4: /cgn2_6/ptodata1/1/aa/6B.COMB.pep:*
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6: /cgn2_6/ptodata1/1/aa/backfile1.pep:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed.
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	32	88.9	521	4	US-09-071-035-64	Sequence 64, Appl
2	32	88.9	542	4	US-09-071-035-62	Sequence 62, Appl
3	30	83.3	766	4	US-09-463-238-6	Sequence 6, Appl
4	28	77.8	288	2	US-08-424-641B-11	Sequence 11, Appl
5	28	77.8	288	2	US-08-820-980-11	Sequence 11, Appl
6	28	77.8	288	2	US-08-826-439-11	Sequence 11, Appl
7	27	75.0	55	4	US-09-227-357-553	Sequence 553, App
8	27	75.0	77	4	US-09-227-357-552	Sequence 552, App
9	27	75.0	174	2	US-08-683-262B-42	Sequence 42, Appl
10	27	75.0	174	4	US-09-361-707-42	Sequence 42, Appl
11	27	75.0	190	2	US-08-462-481-5	Sequence 5, Appl
12	27	75.0	190	2	US-08-436-771-7	Sequence 7, Appl
13	27	75.0	190	2	US-08-434-998-7	Sequence 7, Appl
14	27	75.0	190	2	US-08-487-797-7	Sequence 7, Appl
15	27	75.0	190	2	US-08-701-005A-5	Sequence 5, Appl
16	27	75.0	190	2	US-08-479-895-5	Sequence 5, Appl
17	27	75.0	190	5	PCT-US95-02058-7	Sequence 7, Appl
18	27	75.0	344	3	US-08-733-837B-6	Sequence 6, Appl
19	27	75.0	371	2	US-08-378-617A-12	Sequence 12, Appl
20	27	75.0	394	1	US-07-914-281-4	Sequence 4, Appl
21	27	75.0	394	1	US-08-393-246-4	Sequence 4, Appl
22	27	75.0	394	1	US-08-525-058A-4	Sequence 4, Appl
23	27	75.0	394	2	US-08-696-731-4	Sequence 4, Appl
24	27	75.0	394	4	US-09-042-531-4	Sequence 4, Appl
25	27	75.0	394	4	US-08-379-040-2	Sequence 2, Appl
26	27	75.0	394	5	PCT-US91-00899-9	Sequence 9, Appl
27	27	75.0	476	3	US-09-188-579-114	Sequence 114, App

28	27	75.0	476	4	US-09-315-444-114	Sequence 114, App
29	27	75.0	476	4	US-09-134-218-6	Sequence 6, Appl
30	27	75.0	476	4	US-09-721-362-114	Sequence 114, App
31	27	75.0	590	4	US-09-332-191-25	Sequence 25, Appl
32	27	75.0	590	4	US-09-232-200-75	Sequence 75, Appl
33	27	75.0	590	4	US-09-232-197-75	Sequence 75, Appl
34	27	75.0	590	4	US-09-232-201-75	Sequence 29, Appl
35	27	75.0	650	4	US-09-232-191-29	Sequence 75, Appl
36	27	75.0	650	4	US-09-232-200-79	Sequence 75, Appl
37	27	75.0	650	4	US-09-232-197-79	Sequence 97, Appl
38	27	75.0	650	4	US-09-232-197-97	Sequence 97, Appl
39	27	75.0	650	4	US-09-232-201-79	Sequence 97, Appl
40	27	75.0	650	4	US-09-232-201-97	Sequence 6, Appl
41	27	75.0	1288	3	US-08-762-428A-6	Sequence 56, Appl
42	27	75.0	14	6	5164485-4	Sequence 122, App
43	26	72.2	19	4	US-08-818-112-56	
44	26	72.2	19	4	US-08-818-112-122	
45	26	72.2	19	4	US-08-818-112-122	

ALIGNMENTS

RESULT 1
US-09-071-035-64
Sequence 64, Application US/09071035
Patent No. 6448043
GENERAL INFORMATION:
APPLICANT: Gil H. Choi
TITLE OF INVENTION: Enterococcus faecalis Polynucleotides and Polypeptides
NUMBER OF SEQUENCES: 496
CORRESPONDENCE ADDRESSES:
ADDRESSEE: Human Genome Sciences, Inc.
STREET: 9410 Key West Avenue
CITY: Rockville
STATE: Maryland
COUNTRY: USA
ZIP: 20850
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch, 1.44MB storage
COMPUTER: HP Vectra 486/33
OPERATING SYSTEM: MSDOS version 6.2
SOFTWARE: ASCII text
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/071,035
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: A. Anders Brookes
REGISTRATION NUMBER: 36,373
REFERENCE/DOCKET NUMBER: PB369P2
TELECOMMUNICATION INFORMATION:
TELEPHONE: (301) 309-8504
TELEFAX: (301) 309-8512
INFORMATION FOR SEQ ID NO: 64:
SEQUENCE CHARACTERISTICS:
LENGTH: 521 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-071-035-64
Query Match 88.9%, Score 32, DB 4, Length 521;
Best Local Similarity 85.7%, Pred. No. 29;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
OY 1 EKSRTGD 7
DB 405 EKSRTGD 411

RESULT 2
US-09-071-035-62
Sequence 62, Application US/09071035
Patent No. 6448043
GENERAL INFORMATION:
APPLICANT: Gil H. Choi
TITLE OF INVENTION: Enterococcus faecalis Polynucleotides and Polypeptides
NUMBER OF SEQUENCES: 496
CORRESPONDENCE ADDRESS:
ADDRESSEE: Human Genome Sciences, Inc.
STREET: 9410 Key West Avenue
CITY: Rockville
STATE: Maryland
COUNTRY: USA
ZIP: 20850
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 Inch, 1.4MB Storage
COMPUTER: HP Vectra 486/33
OPERATING SYSTEM: MSDOS version 6.2
SOFTWARE: ASCII Text
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/071.035
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: A. Anders Brooks
REGISTRATION NUMBER: 36,373
REFERENCE/DOCKET NUMBER: PB369P2
TELECOMMUNICATION INFORMATION:
TELEPHONE: (301) 309-8504
TELEFAX: (301) 309-8512
INFORMATION FOR SEQ ID NO: 62:
SEQUENCE CHARACTERISTICS:
LENGTH: 542 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-071-035-62

Query Match 88.9%; Score 32; DB 4; Length 542;
Best Local Similarity 85.7%; Pred. No. 30;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 EKSRTGD 7
Db 426 EKSRTGD 432

RESULT 3
US-09-463-238-6
Sequence 6, Application US/09463238
Patent No. 6469230
GENERAL INFORMATION:
APPLICANT: Edwards, Elizabeth A
APPLICANT: Smith, Allison M
APPLICANT: Bustos Guillen, Regia
APPLICANT: Martin, Catherine R
TITLE OF INVENTION: Starch Debranching Enzymes
FILE REFERENCE: 97.118
CURRENT APPLICATION NUMBER: US/09/463.238
CURRENT FILING DATE: 2000-01-21
PRIOR APPLICATION NUMBER: PCT/GB98/02280
PRIOR FILING DATE: 1998-07-30
PRIOR APPLICATION NUMBER: GB 9716185.5
PRIOR FILING DATE: 1997-07-31
NUMBER OF SEQ ID NOS: 30

SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 6
LENGTH: 766
TYPE: PRT
ORGANISM: Solanum tuberosum
US-09-463-238-6

Query Match 83.3%; Score 30; DB 4; Length 766;
Best Local Similarity 71.4%; Pred. No. 11e+02;
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 EKSRTGD 7
Db 141 OKNRRTGD 147

RESULT 4
US-08-424-641B-11
Sequence 11, Application US/08424641B
Patent No. 5824523
GENERAL INFORMATION:
APPLICANT: Sylvain Moineau, Shirley A.
APPLICANT: Walker, Ebenezer R. Vedamuthu,
APPLICANT: and Peter A. Vandenberg
TITLE OF INVENTION: Isolated DNA Encoding
TITLE OF INVENTION: Enzyme For Phage
NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
ADDRESSEE: Ian C. McLeod
STREET: 2190 Commons Parkway
CITY: Okemos
STATE: Michigan
COUNTRY: USA
ZIP: 48864
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 5.25 Inch, 360 Kb
MEDIUM TYPE: storage
COMPUTER: Acer
OPERATING SYSTEM: MS-DOS
SOFTWARE: Wordperfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/424.641B
FILING DATE: April 19, 1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/366,480
FILING DATE: December 30, 1994
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Ian C. McLeod
REGISTRATION NUMBER: 20,931
REFERENCE/DOCKET NUMBER: MT 4.1-151
TELECOMMUNICATION INFORMATION:
TELEPHONE: (517) 347-4100
TELEFAX: (517) 347-4103
TELEFAX: No. 5824523e
INFORMATION FOR SEQ ID NO: 11:
SEQUENCE CHARACTERISTICS:
LENGTH: 288 Amino Acids
TYPE: Amino Acid
STRANDEDNESS: Single
TOPOLOGY: Linear
MOLECULE TYPE: Peptide
US-08-424-641B-11

Query Match 77.8%; Score 28; DB 2; Length 288;
Best Local Similarity 83.3%; Pred. No. 1.2e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 KSRTGD 7
Db 144 KNRTGD 149

RESULT 5
US-08-820-980-11
Sequence 11, Application US/08820980,
Patent No. 5925388
GENERAL INFORMATION:
APPLICANT: Sylvain Moineau, Shirley A.
APPLICANT: Walker, Ebenezer R. Vedamuthu,
APPLICANT: and Peter A. Vandenberg
TITLE OF INVENTION: Isolated DNA Encoding
TITLE OF INVENTION: Enzyme For Phage
TITLE OF INVENTION: Resistance
NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
ADDRESSEE: Ian C. McLeod
STREET: 2190 Commons Parkway
CITY: Okemos
STATE: Michigan
COUNTRY: USA
ZIP: 48864
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 5.25 inch, 360 Kb
MEDIUM TYPE: storage
COMPUTER: Acer
OPERATING SYSTEM: MS-DOS
SOFTWARE: Wordperfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/820,980
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/424,641
FILING DATE: April 19, 1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Ian C. McLeod
REGISTRATION NUMBER: 20,931
REFERENCE/DOCKET NUMBER: Quest 4.1-156
TELECOMMUNICATION INFORMATION:
TELEPHONE: (517) 347-4100
TELEFAX: (517) 347-4103
TELEX: No. 5925388e
INFORMATION FOR SEQ ID NO: 11:
SEQUENCE CHARACTERISTICS:
LENGTH: 288 Amino Acids
TYPE: Amino Acid
STRANDEDNESS: Single
TOPOLOGY: Linear
MOLECULE TYPE: Peptide
US-08-820-980-11

Query Match 77.8%; Score 28; DB 2; Length 288;
Best Local Similarity 83.3%; Pred. No. 1.2e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 2 KSRMGD 7
DB 144 KNRMGD 149

RESULT 6
US-08-826-439-11
Sequence 11, Application US/08826439
Patent No. 5972673
GENERAL INFORMATION:
APPLICANT: Sylvain Moineau, Shirley A.
APPLICANT: Walker, Ebenezer R. Vedamuthu,
APPLICANT: and Peter A. Vandenberg
TITLE OF INVENTION: Isolated DNA Encoding
TITLE OF INVENTION: Enzyme For Phage
TITLE OF INVENTION: Resistance
NUMBER OF SEQUENCES: 12

CORRESPONDENCE ADDRESS:
ADDRESSEE: Ian C. McLeod
STREET: 2190 Commons Parkway
CITY: Okemos
STATE: Michigan
COUNTRY: USA
ZIP: 48864
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 5.25 inch, 360 Kb
MEDIUM TYPE: storage
COMPUTER: Acer
OPERATING SYSTEM: MS-DOS
SOFTWARE: Wordperfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/826,439
FILING DATE:
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/424,641
FILING DATE: April 19, 1995
CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: Ian C. McLeod
REGISTRATION NUMBER: 20,931
REFERENCE/DOCKET NUMBER: Quest 4.1-155
TELECOMMUNICATION INFORMATION:
TELEPHONE: (517) 347-4100
TELEFAX: (517) 347-4103
TELEX: No. 5972673e
INFORMATION FOR SEQ ID NO: 11:
SEQUENCE CHARACTERISTICS:
LENGTH: 288 Amino Acids
TYPE: Amino Acid
STRANDEDNESS: Single
TOPOLOGY: Linear
MOLECULE TYPE: Peptide
US-08-826-439-11

Query Match 77.8%; Score 28; DB 2; Length 288;
Best Local Similarity 83.3%; Pred. No. 1.2e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 2 KSRMGD 7
DB 144 KNRMGD 149

RESULT 7
US-09-227-357-553
Sequence 553, Application US/09227357
Patent No. 6342581
GENERAL INFORMATION:
APPLICANT: Fischer et al.
TITLE OF INVENTION: 123 Human Secreted Proteins
FILE REFERENCE: P2010P1
CURRENT APPLICATION NUMBER: US/09/227,357
CURRENT FILING DATE: 1999-01-08
EARLIER APPLICATION NUMBER: PCT/US98/13684
EARLIER FILING DATE: 1998-07-07
EARLIER APPLICATION NUMBER: 60/051,926
EARLIER FILING DATE: 1997-07-08
EARLIER APPLICATION NUMBER: 60/052,793
EARLIER FILING DATE: 1997-07-08
EARLIER APPLICATION NUMBER: 60/051,925
EARLIER FILING DATE: 1997-07-08
EARLIER APPLICATION NUMBER: 60/051,929
EARLIER FILING DATE: 1997-07-08
EARLIER APPLICATION NUMBER: 60/052,803
EARLIER FILING DATE: 1997-07-08
EARLIER APPLICATION NUMBER: 60/052,732
EARLIER FILING DATE: 1997-07-08
EARLIER APPLICATION NUMBER: 60/051,931
EARLIER FILING DATE: 1997-07-08

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: EARLIER APPLICATION NUMBER: 60/051,932
: EARLIER FILING DATE: 1997-07-08
: EARLIER APPLICATION NUMBER: 60/051,916
: EARLIER FILING DATE: 1997-07-08
: EARLIER APPLICATION NUMBER: 60/051,930
: EARLIER FILING DATE: 1997-07-08
: EARLIER APPLICATION NUMBER: 60/051,918
: EARLIER FILING DATE: 1997-07-08
: EARLIER APPLICATION NUMBER: 60/051,920
: EARLIER FILING DATE: 1997-07-08
: EARLIER APPLICATION NUMBER: 60/052,733
: EARLIER FILING DATE: 1997-07-08
: EARLIER APPLICATION NUMBER: 60/052,795
: EARLIER FILING DATE: 1997-07-08
: EARLIER APPLICATION NUMBER: 60/051,919
: EARLIER FILING DATE: 1997-07-08
: EARLIER APPLICATION NUMBER: 60/051,928
: EARLIER FILING DATE: 1997-07-08
: EARLIER APPLICATION NUMBER: 60/055,722
: EARLIER FILING DATE: 1997-08-18
: EARLIER APPLICATION NUMBER: 60/055,723
: EARLIER FILING DATE: 1997-08-18
: EARLIER APPLICATION NUMBER: 60/055,948
: EARLIER FILING DATE: 1997-08-18
: EARLIER APPLICATION NUMBER: 60/055,949
: EARLIER FILING DATE: 1997-08-18
: EARLIER APPLICATION NUMBER: 60/055,953
: EARLIER FILING DATE: 1997-08-18
: EARLIER APPLICATION NUMBER: 60/055,950
: EARLIER FILING DATE: 1997-08-18
: EARLIER APPLICATION NUMBER: 60/055,947
: EARLIER FILING DATE: 1997-08-18
: EARLIER APPLICATION NUMBER: 60/055,964
: EARLIER FILING DATE: 1997-08-18
: EARLIER APPLICATION NUMBER: 60/056,360
: EARLIER FILING DATE: 1997-08-18
: EARLIER APPLICATION NUMBER: 60/055,684
: EARLIER FILING DATE: 1997-08-18
: EARLIER APPLICATION NUMBER: 60/055,984
: EARLIER FILING DATE: 1997-08-18
: EARLIER APPLICATION NUMBER: 60/055,954
: EARLIER FILING DATE: 1997-08-18
: EARLIER APPLICATION NUMBER: 60/058,785
: EARLIER FILING DATE: 1997-09-12
: EARLIER APPLICATION NUMBER: 60/058,664
: EARLIER FILING DATE: 1997-09-12
: EARLIER APPLICATION NUMBER: 60/058,660
: EARLIER FILING DATE: 1997-09-12
: EARLIER APPLICATION NUMBER: 60/058,661
: EARLIER FILING DATE: 1997-09-12
: NUMBER OF SEQ ID NOS: 672
: SOFTWARE: PatentIn Ver. 2.0
: SEQ ID NO 553
: LENGTH: 55
: TYPE: PRT
: ORGANISM: Homo sapiens
US-09-227-357-553

Query Match      75.08; Score 27; DB 4; Length 55;
Best Local Similarity 83.38; Pred. No. 37;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      2 KSRGCD 7
       1 11111
Db      7 KDRGCD 12

RESULT 8
US-09-227-357-552
: Sequence 552, Application US/09227357
: Patent No. 6342381
: GENERAL INFORMATION:
: APPLICANT: Fischer et al.
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: TITLE OF INVENTION: 123 Human Secreted Proteins
: FILE REFERENCE: P2010P1
: CURRENT APPLICATION NUMBER: US/09/227,357
: CURRENT FILING DATE: 1999-01-08
: EARLIER APPLICATION NUMBER: PCT/US98/13684
: EARLIER FILING DATE: 1998-07-07
: EARLIER APPLICATION NUMBER: 60/051,926
: EARLIER FILING DATE: 1997-07-08
: EARLIER APPLICATION NUMBER: 60/052,793
: EARLIER FILING DATE: 1997-07-08
: EARLIER APPLICATION NUMBER: 60/051,925
: EARLIER FILING DATE: 1997-07-08
: EARLIER APPLICATION NUMBER: 60/051,929
: EARLIER FILING DATE: 1997-07-08
: EARLIER APPLICATION NUMBER: 60/052,803
: EARLIER FILING DATE: 1997-07-08
: EARLIER APPLICATION NUMBER: 60/052,732
: EARLIER FILING DATE: 1997-07-08
: EARLIER APPLICATION NUMBER: 60/051,931
: EARLIER FILING DATE: 1997-07-08
: EARLIER APPLICATION NUMBER: 60/051,932
: EARLIER FILING DATE: 1997-07-08
: EARLIER APPLICATION NUMBER: 60/051,916
: EARLIER FILING DATE: 1997-07-08
: EARLIER APPLICATION NUMBER: 60/051,930
: EARLIER FILING DATE: 1997-07-08
: EARLIER APPLICATION NUMBER: 60/051,918
: EARLIER FILING DATE: 1997-07-08
: EARLIER APPLICATION NUMBER: 60/051,920
: EARLIER FILING DATE: 1997-07-08
: EARLIER APPLICATION NUMBER: 60/052,733
: EARLIER FILING DATE: 1997-07-08
: EARLIER APPLICATION NUMBER: 60/052,795
: EARLIER FILING DATE: 1997-07-08
: EARLIER APPLICATION NUMBER: 60/051,919
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: EARLIER APPLICATION NUMBER: 60/051,928
: EARLIER FILING DATE: 1997-07-08
: EARLIER APPLICATION NUMBER: 60/055,722
: EARLIER FILING DATE: 1997-08-18
: EARLIER APPLICATION NUMBER: 60/055,948
: EARLIER FILING DATE: 1997-08-18
: EARLIER APPLICATION NUMBER: 60/055,949
: EARLIER FILING DATE: 1997-08-18
: EARLIER APPLICATION NUMBER: 60/055,953
: EARLIER FILING DATE: 1997-08-18
: EARLIER APPLICATION NUMBER: 60/055,950
: EARLIER FILING DATE: 1997-08-18
: EARLIER APPLICATION NUMBER: 60/055,947
: EARLIER FILING DATE: 1997-08-18
: EARLIER APPLICATION NUMBER: 60/055,964
: EARLIER FILING DATE: 1997-08-18
: EARLIER APPLICATION NUMBER: 60/056,360
: EARLIER FILING DATE: 1997-08-18
: EARLIER APPLICATION NUMBER: 60/055,684
: EARLIER FILING DATE: 1997-08-18
: EARLIER APPLICATION NUMBER: 60/055,984
: EARLIER FILING DATE: 1997-08-18
: EARLIER APPLICATION NUMBER: 60/055,954
: EARLIER FILING DATE: 1997-08-18
: EARLIER APPLICATION NUMBER: 60/058,785
: EARLIER FILING DATE: 1997-09-12
: EARLIER APPLICATION NUMBER: 60/058,664
: EARLIER FILING DATE: 1997-09-12
: EARLIER APPLICATION NUMBER: 60/058,660
: EARLIER FILING DATE: 1997-09-12
: EARLIER APPLICATION NUMBER: 60/058,661
: EARLIER FILING DATE: 1997-09-12
: NUMBER OF SEQ ID NOS: 672
: SOFTWARE: PatentIn Ver. 2.0
: SEQ ID NO 552
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LENGTH: 77
TYPE: PRT
ORGANISM: Homo sapiens
US-09-227-357-552

Query Match 75.0%; Score 27; DB 4; Length 77;
Best Local Similarity 83.3%; Pred. No. 52;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 KSRTGD 7
DB 29 KDRTGD 34

RESULT 9
US-08-683-262B-42
Sequence 42, Application US/08683262B
Patent No. 5929220
GENERAL INFORMATION:
APPLICANT: Shuping Tong et al.
TITLE OF INVENTION: HEPADNAVIRUS RECEPTOR
NUMBER OF SEQUENCES: 75
CORRESPONDENCE ADDRESSES:
ADDRESSEE: Fish & Richardson P.C.
STREET: 225 Franklin Street
CITY: Boston
STATE: Massachusetts
COUNTRY: U.S.A.
ZIP: 02110-2804
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/683,262B
FILING DATE: 18-JUL-1996
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Fraser, Janis K.
REGISTRATION NUMBER: 31,819
REFERENCE/DOCKET NUMBER: 00786/287002
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 542-5070
TELEFAX: (617) 542-8906
TELEX: 200154
INFORMATION FOR SEQ ID NO: 42:
SEQUENCE CHARACTERISTICS:
LENGTH: 174 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-683-262B-42

Query Match 75.0%; Score 27; DB 2; Length 174;
Best Local Similarity 83.3%; Pred. No. 1,2e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 KSRTGD 7
DB 165 ESRTGD 170

RESULT 10
US-09-361-707-42
Sequence 42, Application US/09361707
Patent No. 6258357
GENERAL INFORMATION:
APPLICANT: Tong, Shuping
LI, Jisu
Wands, Jack R.
TITLE OF INVENTION: HEP A DNA VIRUS RECEPTOR
NUMBER OF SEQUENCES: 117

CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson P.C.
STREET: 225 Franklin Street
CITY: Boston
STATE: MA
COUNTRY: USA
ZIP: 02110-2804
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSeq for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/361,707
FILING DATE: 27-JUL-1999
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/683,262
FILING DATE: 18-JUL-1996
ATTORNEY/AGENT INFORMATION:
NAME: Creason, Gary L.
REGISTRATION NUMBER: 34,310
REFERENCE/DOCKET NUMBER: 00786/287003
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 542-5070
TELEFAX: (617) 542-8906
INFORMATION FOR SEQ ID NO: 42:
SEQUENCE CHARACTERISTICS:
LENGTH: 174 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 42:
US-09-361-707-42

Query Match 75.0%; Score 27; DB 4; Length 174;
Best Local Similarity 83.3%; Pred. No. 1,2e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 KSRTGD 7
DB 165 ESRTGD 170

RESULT 11
US-08-462-481-5
Sequence 5, Application US/08462481
Patent No. 5840577
GENERAL INFORMATION:
APPLICANT: Silverman, Robert H.
APPLICANT: Zhou, Aimin
TITLE OF INVENTION: Animal 2-5A- Dependent RNases and
TITLE OF INVENTION: Encoding Sequence Therefor
Patent No. 5840577
NUMBER OF SEQUENCES: 5
CORRESPONDENCE ADDRESSES:
ADDRESSEE: Ruden, Barnett, McClosky, Smith, Schuster &
STREET: 200 East Broward Boulevard
CITY: Fort Lauderdale
STATE: Florida
COUNTRY: USA
ZIP: 33301
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/462,481
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/028,086
FILING DATE: 08-MAR-1993
ATTORNEY/AGENT INFORMATION:
NAME: Manso, Peter J.
REGISTRATION NUMBER: 32,264
REFERENCE/DOCKET NUMBER: C111363-13
TELECOMMUNICATION INFORMATION:
TELEPHONE: 305/527/2498
TELEFAX: 305/764/4996
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 190 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-462-481-5

Query Match 75.0%; Score 27; DB 2; Length 190;
Best Local Similarity 71.4%; Pred. No. 1.3e+02;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

OY 1 EKSRTGD 7
11:11
DB 58 EKARTAD 64

RESULT 12
US-08-436-771-7
Sequence 7, Application US/08436771
Patent No. 5861300
GENERAL INFORMATION:
APPLICANT: Silverman, Robert H.
APPLICANT: Sengupta, Dibyendu N.
TITLE OF INVENTION: Antiviral Transgenic Plants, Vectors,
TITLE OF INVENTION: Cells and Methods
NUMBER OF SEQUENCES: 11
CORRESPONDENCE ADDRESS:
ADDRESSEE: Ruden, Barnett, McClosky, Smith, Schuster &
STREET: 200 E. Broward Boulevard
CITY: Fort Lauderdale
STATE: Florida
COUNTRY: USA
ZIP: 33301
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/436,771
FILING DATE:
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/198,973
FILING DATE: 18-FEB-1994
ATTORNEY/AGENT INFORMATION:
NAME: Manso, Peter J.
REGISTRATION NUMBER: 32,264
REFERENCE/DOCKET NUMBER: C111363-16
TELECOMMUNICATION INFORMATION:
TELEPHONE: 305/527/2498
TELEFAX: 305/764/4996
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 190 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-436-771-7

Query Match 75.0%; Score 27; DB 2; Length 190;
Best Local Similarity 71.4%; Pred. No. 1.3e+02;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

OY 1 EKSRTGD 7
11:11
DB 58 EKARTAD 64

RESULT 13
US-08-434-998-7
Sequence 7, Application US/08434998
Patent No. 5866781
GENERAL INFORMATION:
APPLICANT: Silverman, Robert H.
APPLICANT: Sengupta, Dibyendu N.
TITLE OF INVENTION: Antiviral Transgenic Plants, Vectors,
TITLE OF INVENTION: Cells and Methods
NUMBER OF SEQUENCES: 11
CORRESPONDENCE ADDRESS:
ADDRESSEE: Ruden, Barnett, McClosky, Smith, Schuster &
STREET: 200 E. Broward Boulevard
CITY: Fort Lauderdale
STATE: Florida
COUNTRY: USA
ZIP: 33301
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/434,998
FILING DATE:
CLASSIFICATION: 800
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/198,973
FILING DATE: 18-FEB-1994
ATTORNEY/AGENT INFORMATION:
NAME: Manso, Peter J.
REGISTRATION NUMBER: 32,264
REFERENCE/DOCKET NUMBER: C111363-16
TELECOMMUNICATION INFORMATION:
TELEPHONE: 305/527/2498
TELEFAX: 305/764/4996
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 190 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-434-998-7

Query Match 75.0%; Score 27; DB 2; Length 190;
Best Local Similarity 71.4%; Pred. No. 1.3e+02;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

OY 1 EKSRTGD 7
11:11
DB 58 EKARTAD 64

RESULT 14
US-08-487-797-7
Sequence 7, Application US/08487797
Patent No. 5866787
GENERAL INFORMATION:
APPLICANT: Silverman, Robert H.
APPLICANT: Sengupta, Dibyendu N.
TITLE OF INVENTION: Transgenic Plants Co-Expressing A
TITLE OF INVENTION: Functional Human 2-5A System

NUMBER OF SEQUENCES: 11
CORRESPONDENCE ADDRESSES:
ADDRESSEE: Holland & Knight
STREET: One E. Broadway Boulevard, #1300
CITY: Fort Lauderdale
STATE: Florida
COUNTRY: USA
ZIP: 33301
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/487,797
FILING DATE: 07-JUNE-1995
CLASSIFICATION: 800
ATTORNEY/AGENT INFORMATION:
NAME: Manso, Peter J.
REGISTRATION NUMBER: 32,264
REFERENCE/DOCKET NUMBER: C111363-16(C)
TELECOMMUNICATION INFORMATION:
TELEPHONE: 305/468-7811
TELEFAX: 305/463-2030
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 190 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-487-797-7

Query Match
Best Local Similarity 75.0%; Score 27; DB 2; Length 190;
Pred. No. 1.3e+02;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

OY 1 EKSRTGD 7
11:1111
Db 58 EKARTAD 64

RESULT 15
US-08-701-005A-5
Sequence 5, Application US/08701005A
Patent No. 5877019
GENERAL INFORMATION:
APPLICANT: Silverman, Robert H.
APPLICANT: Hassel, Bret A.
APPLICANT: Zhou, Alvin
TITLE OF INVENTION: Animal 2-5A-Dependent RNases and
TITLE OF INVENTION: Encoding Sequence Therefor
Patent No. 5877019
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESSES:
ADDRESSEE: Rothwell, Figg, Ernst & Kurtz
STREET: 555 - 13th Street, N.W., Suite 701 E
CITY: Washington
STATE: DC
COUNTRY: USA
ZIP: 20004
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/701,005A
FILING DATE: 21-AUG-1996
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/141,304
FILING DATE: 22-OCT-1993

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/028,086
FILING DATE: 08-MAR-1993
ATTORNEY/AGENT INFORMATION:
NAME: Jondle, Robert J.
REGISTRATION NUMBER: 33,915
REFERENCE/DOCKET NUMBER: N1255-111
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-783-6040
TELEFAX: 202-783-6031
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 190 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
FRAGMENT TYPE: internal
ORIGINAL SOURCE:
ORGANISM: E. coli
US-08-701-005A-5

Query Match
Best Local Similarity 75.0%; Score 27; DB 2; Length 190;
Pred. No. 1.3e+02;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

OY 1 EKSRTGD 7
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Db 58 EKARTAD 64

Search completed: November 12, 2002, 17:01:41
Job time : 1.96137 secs

GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on: November 12, 2002, 17:00:26 : Search time 0.540773 Seconds
(Without alignments)
186.640 Million cell updates/sec

Title: US-09-848-271-2_COPY_105_111

Perfect score: 36

Sequence: 1 EKSRTGD 7

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Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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Published Applications_AA:*

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14: /cgn2_6/ptodata/1/pubppaa/US60_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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4	28	77.8	50	10	US-09-864-761-37990
5	28	77.8	466	10	US-09-741-669-303
6	28	77.8	762	10	US-09-925-299-998
7	27	75.0	54	10	US-09-867-550-1596
8	27	75.0	144	10	US-09-815-242-11116
9	27	75.0	174	10	US-09-818-066-42
10	27	75.0	359	10	US-09-994-427A-11
11	27	75.0	382	10	US-09-825-414-30
12	27	75.0	394	10	US-09-863-475A-4
13	27	75.0	394	10	US-09-946-034-2
14	27	75.0	590	10	US-09-943-671-25
15	27	75.0	650	10	US-09-943-671-25
16	27	75.0	855	10	US-09-815-242-11930
17	27	75.0	2568	10	US-09-866-108-3
18	26	72.2	68	10	US-09-864-761-42165
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20	26	72.2	170	10	US-09-818-066-49
21	26	72.2	174	10	US-09-818-066-45
22	26	72.2	174	10	US-09-818-066-46
23	26	72.2	174	10	US-09-818-066-47
24	26	72.2	174	10	US-09-818-066-48
25	26	72.2	199	10	US-09-921-640-6
26	26	72.2	212	10	US-09-925-299-968
27	26	72.2	234	10	US-09-915-593-2
28	26	72.2	240	10	US-09-915-593-6
29	26	72.2	241	10	US-09-915-593-4
30	26	72.2	241	10	US-09-915-593-28
31	26	72.2	241	12	US-10-116-378-3
32	26	72.2	258	10	US-09-921-640-9
33	26	72.2	264	10	US-09-925-301-905
34	26	72.2	283	9	US-09-970-989-2
35	26	72.2	307	10	US-09-788-826-20
36	26	72.2	315	10	US-09-739-554-124
37	26	72.2	315	10	US-09-904-615-124
38	26	72.2	372	10	US-09-818-066-64
39	26	72.2	426	10	US-09-864-761-42921
40	26	72.2	469	10	US-09-925-300-1494
41	26	72.2	742	10	US-09-799-777-18
42	26	72.2	760	10	US-09-265-606-2
43	26	72.2	766	10	US-09-795-693-17
44	26	72.2	874	10	US-09-815-242-11809
45	26	72.2	876	10	US-09-815-242-10269

ALIGNMENTS

Sequence 49, App1
Sequence 45, App1
Sequence 46, App1
Sequence 47, App1
Sequence 48, App1
Sequence 6, App1
Sequence 966, App
Sequence 2, App1
Sequence 6, App1
Sequence 4, App1
Sequence 28, App1
Sequence 3, App1
Sequence 9, App1
Sequence 905, App
Sequence 2, App1
Sequence 20, App1
Sequence 124, App
Sequence 64, App1
Sequence 42921, A
Sequence 1494, Ap
Sequence 18, App1
Sequence 2, App1
Sequence 17, App1
Sequence 11809, A
Sequence 10269, A

RESULT 1
US-09-854-864-5
Sequence 5, Application US/09854864
Patent No. US20020081296A1
GENERAL INFORMATION:
APPLICANT: YU, GANG
TITLE OF INVENTION: METHODS AND COMPOSITIONS OF MATTER CONCERNING APRIL/670, BCMA,
TITLE OF INVENTION: BLXS/AGP-3, AND TACTI
FILE REFERENCE: A-686B
CURRENT APPLICATION NUMBER: US/09/854,864
CURRENT FILING DATE: 2001-09-11
PRIOR APPLICATION NUMBER: US 60/204,039
PRIOR FILING DATE: 2000-05-12
PRIOR APPLICATION NUMBER: US 60/214,591
PRIOR FILING DATE: 2000-06-27
NUMBER OF SEQ ID NOS: 31
SOFTWARE: PatentIn version 3.1
SEQ ID NO 5
LENGTH: 181
TYPE: PRT
ORGANISM: Homo sapiens
US-09-854-864-5
Query Match 100.0%; Score 36; DB 10; Length 181;
Best Local Similarity 100.0%; Pred. NO. 0.68;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 EKSRTGD 7
Db 102 EKSRTGD 108
RESULT 2
US-09-815-242-5390
Sequence 5390, Application US/09815242
Patent No. US20020061569A1
GENERAL INFORMATION:
APPLICANT: Haselbeck, Robert
APPLICANT: Ohlssen, Karl L.
APPLICANT: Zyskind, Judith W.
APPLICANT: Wall, Daniel

```
; APPLICANT: Trawick, John D.
; APPLICANT: Carr, Grant J.
; APPLICANT: Yamamoto, Robert T.
; APPLICANT: Xu, H. Howard
; TITLE OF INVENTION: Identification of Essential Genes in
; FILE REFERENCE: ELITRA.011A
; CURRENT APPLICATION NUMBER: US/09/815,242
; CURRENT FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/191,078
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: 60/206,848
; PRIOR FILING DATE: 2000-05-23
; PRIOR APPLICATION NUMBER: 60/207,727
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: 60/242,578
; PRIOR FILING DATE: 2000-10-23
; PRIOR APPLICATION NUMBER: 60/253,625
; PRIOR FILING DATE: 2000-11-27
; PRIOR APPLICATION NUMBER: 60/257,931
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: 60/269,308
; PRIOR FILING DATE: 2001-02-16
; NUMBER OF SEQ ID NOS: 14110
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 5390
; LENGTH: 639
; TYPE: PRT
; ORGANISM: Staphylococcus aureus
; US-09-815-242-5390

Query Match      86.1%; Score 31; DB 10; Length 639;
Best Local Similarity 85.7%; Pred. No. 28;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY      1 EKSRTGD 7
        ||| |||
Db      432 EKSMTGD 438

RESULT 3
US-09-815-242-12304
; Sequence 12304, Application US/09815242
; Patent No. US20020061569A1
; GENERAL INFORMATION:
; APPLICANT: Haseldeck, Robert
; APPLICANT: Onlisen, Karl L.
; APPLICANT: Zyskind, Judith W.
; APPLICANT: Wall, Daniel
; APPLICANT: Trawick, John D.
; APPLICANT: Carr, Grant J.
; APPLICANT: Yamamoto, Robert T.
; APPLICANT: Xu, H. Howard
; TITLE OF INVENTION: Identification of Essential Genes in
; FILE REFERENCE: ELITRA.011A
; CURRENT APPLICATION NUMBER: US/09/815,242
; CURRENT FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/191,078
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: 60/206,848
; PRIOR FILING DATE: 2000-05-23
; PRIOR APPLICATION NUMBER: 60/207,727
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: 60/242,578
; PRIOR FILING DATE: 2000-10-23
; PRIOR APPLICATION NUMBER: 60/253,625
; PRIOR FILING DATE: 2000-11-27
; PRIOR APPLICATION NUMBER: 60/257,931
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: 60/269,308
; PRIOR FILING DATE: 2001-02-16
; NUMBER OF SEQ ID NOS: 14110
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; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 12304
; LENGTH: 646
; TYPE: PRT
; ORGANISM: Staphylococcus aureus
; US-09-815-242-12304

Query Match      86.1%; Score 31; DB 10; Length 646;
Best Local Similarity 85.7%; Pred. No. 28;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY      1 EKSRTGD 7
        ||| |||
Db      429 EKSMTGD 435

RESULT 4
US-09-864-761-37990
; Sequence 37990, Application US/09864761
; Patent No. US20020048763A1
; GENERAL INFORMATION:
; APPLICANT: Penn, Sharron G.
; APPLICANT: Rank, David R.
; APPLICANT: Hanzel, David K.
; APPLICANT: Chen, Wensheng
; TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FO
; FILE REFERENCE: Aeomica-X-1
; CURRENT APPLICATION NUMBER: US/09/864,761
; CURRENT FILING DATE: 2001-05-23
; PRIOR APPLICATION NUMBER: US 60/180,312
; PRIOR FILING DATE: 2000-02-04
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: US 09/632,366
; PRIOR FILING DATE: 2000-08-03
; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00663
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00662
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00661
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00670
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: US 60/234,687
; PRIOR FILING DATE: 2000-09-21
; PRIOR APPLICATION NUMBER: US 09/608,408
; PRIOR FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: US 09/774,203
; PRIOR FILING DATE: 2001-01-29
; NUMBER OF SEQ ID NOS: 49117
; SOFTWARE: Annonmax Sequence Listing Engine vers. 1.1
; SEQ ID NO 37990
; LENGTH: 50
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
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OTHER INFORMATION: MAP TO AP000125.1
OTHER INFORMATION: EXPRESSED IN HEART, SIGNAL = 0.84
OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 0.7
OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 0.57
OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 0.65
OTHER INFORMATION: EST_HUMAN HIT: AUI56079.1, EVALUATE 2.20e+00
US-09-864-761-37990

Query Match 77.8%; Score 28; DB 10; Length 50;
Best Local Similarity 71.4%; Pred. No. 9.3;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

OY 1 EKSRTGD 7
1:1111
DB 33 EKARTGD 39

RESULT 5
US-09-741-669-303
Sequence 303, Application US/09741669
Patent No. US20020022718A1
GENERAL INFORMATION:
APPLICANT: Forsyth, R. Allyn
APPLICANT: Ohlson, Karl L.
APPLICANT: Zyskind, Judith W.
TITLE OF INVENTION: Genes Identified as required for
FILE REFERENCE: ELITRA.009A
CURRENT APPLICATION NUMBER: US/09/741,669
CURRENT FILING DATE: 2000-12-19
PRIOR APPLICATION NUMBER: US 60/173005
PRIOR FILING DATE: 1999-12-23
NUMBER OF SEQ ID NOS: 481
SOFTWARE: FASTSEQ for Windows Version 4.0
SEQ ID NO 303
LENGTH: 466
TYPE: PRT
ORGANISM: Escherichia coli
US-09-741-669-303

Query Match 77.8%; Score 28; DB 10; Length 466;
Best Local Similarity 71.4%; Pred. No. 89;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

OY 1 EKSRTGD 7
1:1111
DB 194 ERSRAGD 200

RESULT 6
US-09-925-299-998
Sequence 998, Application US/09925299
Patent No. US20020055627A1
GENERAL INFORMATION:
APPLICANT: Rosen et al.
TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies
FILE REFERENCE: PA102
CURRENT APPLICATION NUMBER: US/09/925,299
CURRENT FILING DATE: 2001-08-10
PRIOR APPLICATION NUMBER: PCT/US00/05883
PRIOR FILING DATE: 2000-03-08
PRIOR APPLICATION NUMBER: 60/124,270
PRIOR FILING DATE: 1999-03-12
NUMBER OF SEQ ID NOS: 1556
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 998
LENGTH: 762
TYPE: PRT
ORGANISM: Homo sapiens
US-09-925-299-998

Query Match 77.8%; Score 28; DB 10; Length 762;
Best Local Similarity 71.4%; Pred. No. 1.5e+02;

Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
OY 1 EKSRTGD 7
1:1111
DB 9 EGRTGD 15

RESULT 7
US-09-867-550-1596
Sequence 1596, Application US/09867550
Patent No. US20020082206A1
GENERAL INFORMATION:
APPLICANT: Leach, Martin D.
APPLICANT: Mehroban, Fuad
APPLICANT: Conley, Pamela
APPLICANT: Law, Debbie
APPLICANT: Topper, James
TITLE OF INVENTION: No. US20020082206A1 Polynucleotides from Atherogenic Cells a
FILE REFERENCE: 21402-013 (Cura-313)
CURRENT APPLICATION NUMBER: US/09/867,550
CURRENT FILING DATE: 2001-09-20
PRIOR APPLICATION NUMBER: USSN 60/208,427
PRIOR FILING DATE: 2000-05-30
NUMBER OF SEQ ID NOS: 2125
SOFTWARE: FASTSEQ for Windows Version 4.0
SEQ ID NO 1596
LENGTH: 54
TYPE: PRT
ORGANISM: Homo sapiens
US-09-867-550-1596

Query Match 75.0%; Score 27; DB 10; Length 54;
Best Local Similarity 83.3%; Pred. No. 16;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 EKSRTG 6
1:1111
DB 4 ERSRTG 9

RESULT 8
US-09-815-242-11116
Sequence 11116, Application US/09815242
Patent No. US20020061569A1
GENERAL INFORMATION:
APPLICANT: Haselbeck, Robert
APPLICANT: Ohlson, Karl L.
APPLICANT: Zyskind, Judith W.
APPLICANT: Wall, Daniel
APPLICANT: Trawick, John D.
APPLICANT: Carr, Grant J.
APPLICANT: Yamamoto, Robert T.
APPLICANT: Xu, H. Howard
TITLE OF INVENTION: Identification of Essential Genes in
FILE REFERENCE: ELITRA.011A
CURRENT APPLICATION NUMBER: US/09/815,242
CURRENT FILING DATE: 2001-03-21
PRIOR APPLICATION NUMBER: 60/191,078
PRIOR FILING DATE: 2000-03-21
PRIOR APPLICATION NUMBER: 60/206,848
PRIOR FILING DATE: 2000-05-23
PRIOR APPLICATION NUMBER: 60/207,727
PRIOR FILING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: 60/242,578
PRIOR FILING DATE: 2000-10-23
PRIOR APPLICATION NUMBER: 60/253,625
PRIOR FILING DATE: 2000-11-27
PRIOR APPLICATION NUMBER: 60/257,931
PRIOR FILING DATE: 2000-12-22
PRIOR APPLICATION NUMBER: 60/269,308
PRIOR FILING DATE: 2001-02-16

NUMBER OF SEQ ID NOS: 14110
SOFTWARE: FASTSEQ for Windows Version 4.0
SEQ ID NO 1116
LENGTH: 144
TYPE: PRT
ORGANISM: Haemophilus Influenzae
US-09-815-242-11116

Query Match
Best Local Similarity 83.3%; Score 27; DB 10; Length 144;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 EKSRTG 6
DB 38 QKSRTG 43

RESULT 9
US-09-818-066-42
Sequence 42, Application US/09818066
Patent No. US20020032307A1
GENERAL INFORMATION:
APPLICANT: Shuping Tong et al.
TITLE OF INVENTION: HEPADNAVIRUS RECEPTOR
NUMBER OF SEQUENCES: 75
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson P.C.
STREET: 225 Franklin Street
CITY: Boston
STATE: Massachusetts
COUNTRY: U.S.A.
ZIP: 02110-2804
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/818,066
FILING DATE: 27-Mar-2001
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/683,262
FILING DATE: 18-JUL-1996
ATTORNEY/AGENT INFORMATION:
NAME: Fraser, Janis K.
REGISTRATION NUMBER: 31,819
REFERENCE/DOCKET NUMBER: 00786/287002
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 542-5070
TELEFAX: (617) 542-8906
TELEX: 200154
INFORMATION FOR SEQ ID NO: 42:
SEQUENCE CHARACTERISTICS:
LENGTH: 174 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 42:
US-09-818-066-42

Query Match
Best Local Similarity 75.0%; Score 27; DB 10; Length 174;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 KSRTGD 7
DB 165 ESRSTD 170

RESULT 10
US-09-994-427A-11
Sequence 11, Application US/09994427A

PATENT No. US20020128221A1
GENERAL INFORMATION:
APPLICANT: Genon Corporation
APPLICANT: Schiff, J. Michael
TITLE OF INVENTION: GLYCOSYLTRANSFERASE VECTORS FOR TREATING CANCER
FILE REFERENCE: 083,002
CURRENT APPLICATION NUMBER: US/09/994,427A
CURRENT FILING DATE: 2002-02-26
PRIOR APPLICATION NUMBER: 60/253,395
PRIOR FILING DATE: 2000-11-27
NUMBER OF SEQ ID NOS: 17
SOFTWARE: Patentin version 3.1
SEQ ID NO 11
LENGTH: 359
TYPE: PRT
ORGANISM: Mus musculus
US-09-994-427A-11

Query Match
Best Local Similarity 71.4%; Score 27; DB 10; Length 359;
Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 EKSRTGD 7
DB 63 EKGRGD 69

RESULT 11
US-09-825-414-30
Sequence 30, Application US/09825414
Patent No. US20020083489A1
GENERAL INFORMATION:
APPLICANT: Collmer, Alan
APPLICANT: Alfano, James R.
TITLE OF INVENTION: DNA MOLECULES AND POLYPEPTIDES OF PSEUDOMONAS SYRINGAE
TITLE OF INVENTION: HRP PATHOGENICITY ISLAND AND THEIR USES
FILE REFERENCE: 19603/3243
CURRENT APPLICATION NUMBER: US/09/825,414
CURRENT FILING DATE: 2001-04-03
PRIOR APPLICATION NUMBER: 60/194,160
PRIOR FILING DATE: 2000-04-03
PRIOR APPLICATION NUMBER: 60/224,604
PRIOR FILING DATE: 2000-08-11
PRIOR APPLICATION NUMBER: 60/249,548
PRIOR FILING DATE: 2000-11-17
NUMBER OF SEQ ID NOS: 91
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 30
LENGTH: 382
TYPE: PRT
ORGANISM: Pseudomonas syringae
US-09-825-414-30

Query Match
Best Local Similarity 75.0%; Score 27; DB 10; Length 382;
Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 EKSRTGD 7
DB 197 EKGRGD 203

RESULT 12
US-09-863-475A-4
Sequence 4, Application US/09863475A
Patent No. US20020102688A1
GENERAL INFORMATION:
APPLICANT: Lowe, John B.
TITLE OF INVENTION: METHODS AND PRODUCTS FOR THE SYNTHESIS
OF OLIGOSACCHARIDE STRUCTURES ON GLYCOPROTEINS,
GLYCOLIPIDS, OR AS FREE MOLECULES, AND FOR THE ISOLATION
OF CLONED GENETIC SEQUENCES THAT DETERMINE THESE STRUCTU

NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:
ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT,
P.C.
STREET: 1755 Jefferson Davis Highway, Fourth Floor
CITY: Arlington
STATE: Virginia
COUNTRY: U.S.A.
ZIP: 22202
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/863,475A
FILING DATE: 24-May-2001
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/914,281
FILING DATE: 20-JUL-1992
ATTORNEY/AGENT INFORMATION:
NAME: Lavalleye, Jean-Paul M. P.
REGISTRATION NUMBER: 31,451
REFERENCE/DOCKET NUMBER: 2363-060-55
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703)521-4500
TELEFAX: (703)521-2347
TELEX: 248855 OPAT UR
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 394 amino acids
TYPE: amino acid
TOPOLOGY: unknown
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 4:
US-09-863-475A-4

Query Match 75.0%; Score 27; DB 10; Length 394;
Best Local Similarity 71.4%; Pred. No. 1.2e+02;
Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 1 EKSRTGD 7
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Db 98 EKRNGD 104

RESULT 13
US-09-946-034-2
Sequence 2, Application US/09946034
Patent No. US2002015248A1
GENERAL INFORMATION:
APPLICANT: Cooper, David K.C.
Koren, Eugen
TITLE OF INVENTION: GENETICALLY ENGINEERED ANIMALS FOR USE
AS ORGAN DONORS
NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
ADDRESSEE: Patrea L. Pabst
STREET: 1100 Peachtree Street, Suite 2800
CITY: Atlanta
STATE: GA
COUNTRY: USA
ZIP: 30309-4530
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/946,034
FILING DATE: 04-Sep-2001
CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/049,817
FILING DATE: 20-APR-1993
ATTORNEY/AGENT INFORMATION:
NAME: Pabst, Patrea L.
REGISTRATION NUMBER: 31,284
REFERENCE/DOCKET NUMBER: BMC100
TELECOMMUNICATION INFORMATION:
TELEPHONE: (404)-815-6508
TELEFAX: (404)-815-6555
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 394 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: NO
ORIGINAL SOURCE:
ORGANISM: Mus musculus
SEQUENCE DESCRIPTION: SEQ ID NO: 2:
US-09-946-034-2

Query Match 75.0%; Score 27; DB 10; Length 394;
Best Local Similarity 71.4%; Pred. No. 1.2e+02;
Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 1 EKSRTGD 7
|||
Db 98 EKRNGD 104

RESULT 14
US-09-943-671-25
Sequence 25, Application US/09943671
Patent No. US2002010673A1
GENERAL INFORMATION:
APPLICANT: Stahl, Andreas
APPLICANT: Hirsch, Andreas
APPLICANT: Lotzsh, Harvey F.
TITLE OF INVENTION: Fatty Acid Transport Proteins
FILE REFERENCE: WH197-21p3ME
CURRENT APPLICATION NUMBER: US/09/943,671
CURRENT FILING DATE: 2001-08-31
PRIOR APPLICATION NUMBER: 09/232,191
PRIOR FILING DATE: 1999-10-14
PRIOR APPLICATION NUMBER: 60/093,491
PRIOR FILING DATE: 1998-07-20
PRIOR APPLICATION NUMBER: 60/110,941
PRIOR FILING DATE: 1998-12-04
NUMBER OF SEQ ID NOS: 37
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 25
LENGTH: 590
TYPE: PPT
ORGANISM: Drosophila melanogaster
US-09-943-671-25

Query Match 75.0%; Score 27; DB 10; Length 590;
Best Local Similarity 83.3%; Pred. No. 1.8e+02;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 2 KSRTGD 7
||||
Db 450 KDRTGD 455

RESULT 15
US-09-943-671-29
Sequence 29, Application US/09943671
Patent No. US2002010673A1
GENERAL INFORMATION:
APPLICANT: Stahl, Andreas

APPLICANT: Hirsch, David J.
APPLICANT: Lodish, Harvey F.
TITLE OF INVENTION: Fatty Acid Transport Proteins
FILE REFERENCE: W197-213ME
CURRENT APPLICATION NUMBER: US/09/943,671
CURRENT FILING DATE: 2001-08-31
PRIOR APPLICATION NUMBER: 09/232,191
PRIOR FILING DATE: 1999-10-14
PRIOR APPLICATION NUMBER: 60/093,491
PRIOR FILING DATE: 1998-07-20
PRIOR APPLICATION NUMBER: 60/110,941
PRIOR FILING DATE: 1998-12-04
NUMBER OF SEQ ID NOS: 37
SOFTWARE: fastSeq for Windows Version 3.0
SEQ ID NO 29
LENGTH: 650
TYPE: PRT
ORGANISM: Caenorhabditis elegans
US-09-943-671-29

Query Match 75.08; Score 27; DB 10; Length 650;
Best Local Similarity 83.38; Pred. No. 2e+02;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 2 KSRTGD 7
1 1111
DB 505 KDRGCD 510

Search completed: November 12, 2002, 17:09:12
Job time : 1.34077 secs

GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on: November 12, 2002, 16:56:36 ; Search time 1.08155 Seconds
(without alignments)
622.203 Million cell updates/sec

Title: US-09-848-271-2_COPY_105_111

Perfect score: 36

Sequence: 1 EKSRTGD 7

Scoring table: BLOSUM62

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Searched: 283224 segs, 96134422 residues

Total number of hits satisfying chosen parameters: 283224

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

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2: pIr2:*
3: pIr3:*
4: pIr4:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	36	100.0	184	2 S43486	B-cell maturation
2	33	91.7	585	2 A69829	ABC transporter (A
3	32	88.9	862	2 A05028	RPCC protein homol
4	32	88.9	1163	2 S07137	DNA-directed RNA p
5	32	88.9	1361	2 A29959	DNA-directed RNA p
6	31	86.1	646	2 H89843	hypothetical prote
7	31	86.1	1195	2 E96615	hypothetical prote
8	30	83.3	92	2 AE3173	transcription regu
9	30	83.3	160	2 C97289	hypothetical prote
10	30	83.3	396	2 AH3650	glycosyl transfera
11	30	83.3	450	2 T04265	probable kasein ki
12	30	83.3	463	2 E72368	asfB/chur-related
13	30	83.3	526	2 S49641	L-galactonolactone
14	29	80.6	149	2 H70441	ribosomal protein
15	29	80.6	316	2 E95307	hypothetical prote
16	29	80.6	583	2 E83794	ABC transporter (A
17	29	80.6	1031	2 C81302	probable type I si
18	28	77.8	111	2 AG1906	photosystem II pr
19	28	77.8	115	2 B69188	nitrogen regulator
20	28	77.8	121	2 S19486	hypothetical prote
21	28	77.8	128	2 E70926	hypothetical prote
22	28	77.8	288	2 B24372	DpnI endonuclease
23	28	77.8	321	2 S35230	hypE protein - Bra
24	28	77.8	324	2 AB2772	inosine-uridine pr
25	28	77.8	371	2 G84398	phosphate transpor
26	28	77.8	378	2 A97552	chain a, crystal s
27	28	77.8	412	2 S69633	hypothetical prote
28	28	77.8	415	2 AB3637	alpha-methylacyl-C
29	28	77.8	421	2 F83400	hypothetical prote

30	28	77.8	466	2 H64904	hypothetical prote
31	28	77.8	482	2 D90983	mannose-1-P guanos
32	28	77.8	482	2 G85828	mannose-1-P guanos
33	28	77.8	529	2 J00783	55.5K sporulation
34	28	77.8	585	2 H83941	ABC transporter (A
35	28	77.8	589	2 H84985	hypothetical prote
36	28	77.8	600	2 S58681	selenocysteine tRN
37	28	77.8	608	2 A53195	afamin precursor -
38	28	77.8	626	2 I38618	zinc finger protei
39	28	77.8	626	2 AF0358	conserved hypotet
40	28	77.8	645	2 T19382	hypothetical prote
41	28	77.8	727	1 A45995	copper-transportin
42	28	77.8	728	2 T36026	ABC excision nucle
43	28	77.8	761	2 T24230	hypothetical prote
44	28	77.8	832	2 S76815	hypothetical prote
45	28	77.8	1025	2 A82516	type I restriction

ALIGNMENTS

RESULT 1
S43486
B-cell maturation factor - human
N:Alternate names: BCM protein; BCMa protein; BEL protein
C:Species: Homo sapiens (man)
C:Date: 27-Jan-1995 #sequence_revision 27-Jan-1995 #text_change 21-Jul-2000
C:Accession: S43486; S31208; S36661
R:Laabl, Y.; Gras, M.P.; Brouet, J.C.; Berger, R.; Larsen, C.J.; Tsapis, A.
Nucleic Acids Res. 22, 1147-1154, 1994
A:Title: The BCMa gene, preferentially expressed during B lymphoid maturation, is bld
A:Reference number: S43486; MUID:94218235; PMID:8165126
A:Accession: S43486
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-184 <LA>
A:Cross-references: EMBL:Z29574; NID:9471244; PIDN:CA82690.1; PID:9471245
R:Laabl, Y.; Gras, M.P.; Carbonnel, F.; Brouet, J.C.; Berger, R.; Larsen, C.J.; Tsapi
EMBO J. 11, 3897-3904, 1992
A:Title: A new gene, BCM, on chromosome 16 is fused to the interleukin 2 gene by a t
A:Reference number: S31208; MUID:93010984; PMID:1356583
A:Accession: S31208
A:Molecule type: mRNA
A:Residues: 1-184 <LA>
A:Cross-references: EMBL:Z14954; NID:929407; PIDN:CAA78679.1; PID:929408
A:Accession: S36661
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 4-184 <LA>
A:Cross-references: EMBL:Z14955
C:Genetics:
A:Gene: GDB:BCMA
A:Cross-references: GDB:135977; OMIM:109545
A:Map position: 16p13.1-16p13.1
A:Introns: 44/1; 93/1
C:Superfamily: human B-cell maturation factor

Query Match 100.0%; Score 36; DB 2; Length 184;
Best local Similarity 100.0%; Pred. No. 1.1;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EKSRTGD 7
DB 105 EKSRTGD 111

RESULT 2
A69829
ABC transporter (ATP-binding protein) homolog yhei - Bacillus subtilis
C:Species: Bacillus subtilis
C:Date: 05-Dec-1997 #sequence_revision 05-Dec-1997 #text_change 02-Feb-2001
C:Accession: A69829
R:Kunst, F.; Ogasawara, N.; Moszer, I.; Albertini, A.M.; Alloni, G.; Azevedo, V.; Ber

C.: Bron, S.; Brouillet, S.; Bruschi, C.V.; Caldwell, B.; Capuano, V.; Carter, N.M.; Chd A.; Ehrlich, S.D.; Emmerson, P.T.; Enlian, K.D.; Errington, J.; Fabel, C.; Ferrari, E. Nature 390, 249-256, 1997

A:Authors: Foulger, D.; Fritze, C.; Fujita, M.; Fujita, Y.; Fuma, S.; Gallizi, A.; Gallier, J.; Harwood, C.R.; Henaut, A.; Hilbert, H.; Holsappel, S.; Hosono, S.; Hullo, M.F.; Koetter, P.; Koningsveld, G.; Krogh, S.; Kumano, M.; Kurita, K.; Lapidus, A.; Lardinois, A.; Luthers, J.; Lazarevic, V.; Lee, S.M.; Levine, A.; Liu, H.; Masuda, S.; Maueel Y. M.; Ogawa, K.; Ogihara, A.; Oudega, B.; Park, S.H.; Parro, V.; Pohl, T.M.; Portetelli Rieger, M.; Rivolta, C.; Roche, E.; Roche, R.; Rosc, M.; Sadele, Y.; Sato, T.; Scanlon, A.; Schelch, S.; Schroeter, R.; Scoffone, F.; Sekiguchi, J.; Sekowska, A.; Seton, A.; Shinozaki, K.; Tamakoshi, A.; Tanaka, T.; Terpstra, P.; Toynon, A.; Tosato, V.; Uchiyama, T.; Winters, P.; Wipit, A.; Yamamoto, H.; Yamane, K.; Yasumoto, K.; Yata, K.; Yoshida, K. A:Authors: Yoshikawa, H.F.; Zumbstein, E.; Yoshikawa, H.; Danchin, A.

A:Title: The complete genome sequence of the Gram-positive bacterium *Bacillus subtilis*. A:Accession: A69580; MUID:98044033; PMID:9384377

A:Accession: A69829

A:Status: preliminary; nucleic acid sequence not shown; translation not shown

A:Molecule type: DNA

A:Residues: 1-585 <KUN>

A:Cross-references: GB:299109; GB:AL009126; NID:92633260; PIDN:CAM12810.1; PID:92633306

A:Experimental source: strain 168

C:Genetics:

A:Gene: yheI

C:Superfamily: Escherichia coli ABC transporter mda; ATP-binding cassette homology

C:Keywords: ATP; nucleotide binding; P-loop

F:354-548/Domain: ATP-binding cassette homology <ABC>

F:371-378/Region: nucleotide-binding motif A (P-loop)

Query Match 91.7%; Score 33; DB 2; Length 585;
Best Local Similarity 85.7%; Pred. No. 18;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 EKSRTGD 7
|||||
DB 110 EKNRTGD 116

RESULT 3

A05028

ProC protein homolog - common tobacco chloroplast

C:Species: chloroplast Nicotiana tabacum (common tobacco)

C:Date: 05-Jun-1987 #sequence_revision 05-Jun-1987 #text_change 11-Apr-1995

C:Accession: A05028

R: Sugita, M.

Submitted to the EMBL Data Library, August 1986

A:Reference number: A00149

A:Molecule type: DNA

A:Accession: A05028

A:Residues: 1-862 <SUG>

A:Experimental source: cv. Bright Yellow 4

R: Shinozaki, K.; Ohme, M.; Tanaka, M.; Wakasugi, T.; Hayashida, N.; Matsubayashi, T.; Z. Deno, H.; Kamogashira, T.; Yamada, K.; Kusuda, J.; Takakawa, F.; Kato, A.; Tohond, N.; Sh. EMBL J. 5, 2043-2049, 1986

A:Title: The complete nucleotide sequence of the tobacco chloroplast genome: its gene or

A:Reference number: A38013

A:Contents: annotation; gene organization, sites, features

C:Genetics:

A:Genome: chloroplast

A:Start codon: TTC

C:Superfamily: chloroplast DNA-directed RNA polymerase beta'-2 chain

C:Keywords: chloroplast

Query Match 88.9%; Score 32; DB 2; Length 862;
Best Local Similarity 85.7%; Pred. No. 47;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 EKSRTGD 7
|||||
DB 609 EKSRTGD 615

RESULT 4

S07137

DNA-directed RNA polymerase (EC 2.7.7.6) beta'-2 chain - garden pea chloroplast (frag

C:Species: chloroplast Pisum sativum (garden pea)

C:Date: 31-Dec-1990 #sequence_revision 31-Dec-1990 #text_change 18-Jun-1999

C:Accession: S07137

R: Cozens, A.L.; Walker, J.E.

Biochem. J. 236, 453-460, 1986

A:Title: Pea chloroplast DNA encodes homologues of Escherichia coli ribosomal subunit

A:Reference number: S07137; MUID:86323089; PMID:3530249

A:Accession: S07137

A:Molecule type: DNA

A:Residues: 1-1163 <COZ>

A:Cross-references: EMBL:X03912; NID:912137; PIDN:CAA27545.1; PID:9829325

C:Genetics:

A:Gene: rpoC2

C:Superfamily: chloroplast DNA-directed RNA polymerase beta'-2 chain

C:Keywords: chloroplast; nucleotidyltransferase; transcription

Query Match 88.9%; Score 32; DB 2; Length 1163;
Best Local Similarity 85.7%; Pred. No. 65;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 EKSRTGD 7
|||||
DB 924 EKSRTGD 930

RESULT 5

A29959

DNA-directed RNA polymerase (EC 2.7.7.6) beta'-2 chain - spinach chloroplast

C:Species: chloroplast Spinacia oleracea (spinach)

C:Date: 15-Dec-1988 #sequence_revision 15-Dec-1988 #text_change 18-Jun-1999

C:Accession: A29959

R: Hudson, G.S.; Holton, T.A.; Whitfield, P.R.; Bottomley, W.

J. Mol. Biol. 200, 639-654, 1988

A:Title: Spinach chloroplast ProC genes encode three subunits of the chloroplast RNA

A:Reference number: A29959; MUID:88316931; PMID:3043524

A:Accession: A29959

A:Molecule type: DNA

A:Residues: 1-1361 <HUD>

A:Cross-references: EMBL:M55297; NID:9295119; PIDN:AAA4639.1; PID:9295122

C:Genetics:

A:Gene: rpoC-2

C:Superfamily: chloroplast DNA-directed RNA polymerase beta'-2 chain

C:Keywords: chloroplast; nucleotidyltransferase; transcription

Query Match 88.9%; Score 32; DB 2; Length 1361;
Best Local Similarity 85.7%; Pred. No. 77;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 EKSRTGD 7
|||||
DB 1123 EKSRTGD 1129

RESULT 6

H89843

hypothetical protein SA0674 [imported] - staphylococcus aureus (strain N315)

C:Species: Staphylococcus aureus

C:Date: 10-May-2001 #sequence_revision 10-May-2001 #text_change 22-Oct-2001

C:Accession: H89843

R: Kuroda, M.; Ohta, T.; Uchiyama, I.; Baba, T.; Yuzawa, H.; Kobayashi, I.; Cui, L.; O. Ma, A.; Mizutani-Oi, Y.; Kobayashi, N.; Sawano, T.; Inoue, R.; Kaito, C.; Sekimizu, K.

C.: Shiba, T.; Hattori, M.; Ogasawara, N.; Hayashi, H.; Hiratsugu, K.

Lancet 357, 1225-1240, 2001

A:Title: Whole genome sequencing of methicillin-resistant Staphylococcus aureus.

A:Reference number: A89758; MUID:21311952; PMID:11418146

A:Accession: H89843

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-646 <KUN>

A:Cross-references: GB:BA000018; PID:913700610; PIDN:BAB41907.1; GSPDB:GN00149

A:Experimental source: strain N315
C:Genetics:
A:Gene: SA0674
C:Superfamily: Bacillus subtilis probable anion-binding protein yf1e

Query Match 86.1%; Score 31; DB 2; Length 646;
Best Local Similarity 85.7%; Pred. No. 59;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 EKSRTGD 7
DB 429 EKSRTGD 435

RESULT 7
E96615
hypothetical protein F16M2.3 [imported] - Arabidopsis thaliana
C:Species: Arabidopsis thaliana (mouse-ear cress)
C>Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 31-Mar-2001
C:Accession: E96615

R:Theologos, A.; Becker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso,
Chin, C.W.; Hughes, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, K.;
ansen, N.F.; Hughes, B.; Hultzer, L.
Nature 408, 816-820, 2000

A:Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C.
C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Malt, R.; Marziani,
Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.
A:Authors: Salberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon,
ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.
A>Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.

A:Reference number: A86141; MUID:21016719; PMID:11130712

A:Accession: E96615

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-1195 <STO>

A:Cross-references: GB:AE005173; NID:g11055842; PIDN:AA628310.1; GSPDB:GN00141

C:Genetics:

A:Gene: F16M2.3

A:Map position: 1

Query Match 86.1%; Score 31; DB 2; Length 1195;
Best Local Similarity 85.7%; Pred. No. 11e+02;

Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 EKSRTGD 7
DB 212 EKSRTGD 218

RESULT 8
AE3173
transcription regulator Atu5113 [imported] - Agrobacterium tumefaciens (strain C58, Dupc
C:Species: Agrobacterium tumefaciens
C>Date: 11-Jan-2002 #sequence_revision 11-Jan-2002 #text_change 11-Jan-2002
C:Accession: AE3173

R:Wood, D.W.; Setubal, J.C.; Kaul, R.; Monks, D.; Chen, L.; Wood, G.E.; Chen, Y.; Woo, L.
erge, G.; Gillet, W.; Grant, S.; Guenther, D.; Kubyavin, T.; Levy, R.; Li, M.; Mclell
; Karp, P.; Romero, P.; Zhang, S.
Science 294, 2317-2323, 2001

A:Authors: Yoo, H.; Tao, Y.; Biddle, P.; Jung, M.; Krespan, W.; Perry, M.; Gordon-Kamm,
ster, E.W.
A>Title: The Genome of the Natural Genetic Engineer Agrobacterium tumefaciens C58.

A:Reference number: AB2577; PMID:11743193

A:Accession: AE3173

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-92 <KUR>

A:Cross-references: GB:AE008687; PIDN:AA145803.1; PID:g17743541; GSPDB:GN00188

A:Experimental source: strain C58 (Dupont)

C:Genetics:

A:Gene: Atu5113

A:Genome: plasmid

Query Match 83.3%; Score 30; DB 2; Length 92;
Best Local Similarity 71.4%; Pred. No. 12;
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 EKSRTGD 7
DB 21 EKSRTGD 27

RESULT 9
C97289

hypothetical protein CAC3165 [imported] - Clostridium acetobutylicum

C:Species: Clostridium acetobutylicum

C>Date: 14-Sep-2001 #sequence_revision 14-Sep-2001 #text_change 14-Sep-2001

C:Accession: C97289

R:Molling, J.; Breton, G.; Omelchenko, M.V.; Markova, K.S.; Zeng, Q.; Gibson, R.;
; Daly, M.J.; Bennett, G.N.; Koonin, E.V.; Smith, D.R.
J. Bacteriol. 183, 4823-4838, 2001

A>Title: Genome Sequence and Comparative Analysis of the Solvent-Producing Bacterium
A:Reference number: A96900; MUID:21359325; PMID:21359325

A:Accession: C97289

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-160 <KUR>

A:Cross-references: GB:AE001437; PIDN:AAK81102.1; PID:g15026232; GSPDB:GN00168

A:Experimental source: Clostridium acetobutylicum ATCC824

C:Genetics:

A:Gene: CAC3165

Query Match 83.3%; Score 30; DB 2; Length 160;
Best Local Similarity 100.0%; Pred. No. 22;

Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EKSRTG 6
DB 51 EKSRTG 56

RESULT 10
AH3650

glycosyl transferase (EC 2.4.1.-) [imported] - Brucella melitensis (strain 16M)

C:Species: Brucella melitensis

C>Date: 01-Feb-2002 #sequence_revision 01-Feb-2002 #text_change 01-Feb-2002

C:Accession: AH3650

R:DelVecchio, V.G.; Kapral, V.; Redkar, R.J.; Patra, G.; Mufer, C.; Los, T.; Ivano
; Mazur, M.; Goldsman, E.; Selkov, E.; Elzer, P.H.; Hagius, S.; O'Callaghan, D.; Le
Proc. Natl. Acad. Sci. U.S.A. 99, 443-448, 2002

A>Title: The genome sequence of the facultative intracellular pathogen Brucella meli

A:Reference number: A03252; PMID:11756688

A:Accession: AH3650

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-356 <KUR>

A:Cross-references: GB:AE008918; PIDN:AA154371.1; PID:g17985355; GSPDB:GN00191

A:Experimental source: strain 16M

C:Genetics:

A:Gene: BME11129

A:Map position: 11

C:Keywords: glycosyltransferase; hexosyltransferase

Query Match 83.3%; Score 30; DB 2; Length 396;
Best Local Similarity 85.7%; Pred. No. 59;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 EKSRTGD 7
DB 352 EKSRTGD 358

RESULT 11
T04265

probable casein kinase (EC 2.7.1.-) - Arabidopsis thaliana

N:Alternate names: protein F20B18.210

C:Species: Arabidopsis thaliana (mouse-ear cress)
C>Date: 30-Apr-1999 #sequence_revision 30-Apr-1999 #text_change 14-Sep-2001
C/Accession: T04265
R:Bevan, M.; Rose, M.; Hempel, S.; Entlan, K.D.; Hohneset, J.; Mewes, H.W.; Mayer, K.F.X
submitted to the Protein Sequence Database, March 1999
A:Reference number: 215263
A/Accession: T04265
A:Molecule type: DNA
A:Residues: 1-450 <BEV>
A:Cross-references: EMBL:AL049483
A:Experimental source: cultivar Columbia; BAC clone F20B18
C:Genetics:
A:Map position: 4
A:Introns: 26/1; 39/3; 63/1; 112/3; 144/3; 168/2; 189/1; 210/2; 238/3; 281/1; 308/3; 330
A>Note: F20B18.210
A:Superfamily: kinase-related transforming protein; protein kinase homology
C:Keywords: phosphotransferase

Query Match 83.3%; Score 30; DB 2; Length 450;
Best Local Similarity 71.4%; Pred. No. 68;
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

OY 1 EKSRTGD 7
Db 403 QRSRTGD 409
:::|||||

RESULT 12
E72268
asEB/cnhr-related protein - Thermotoga maritima (strain MSB8)
C:Species: Thermotoga maritima
C>Date: 11-Jun-1999 #sequence_revision 11-Jun-1999 #text_change 21-Jul-2000
C/Accession: E72268
R:Nelson, K.E.; Clayton, R.A.; Gill, S.R.; Gwinn, M.; Dodson, R.J.; Haft, D.H.; Hickey
Garrett, M.M.; Stewart, A.M.; Cotton, M.D.; Pratt, M.S.; Phillips, C.A.; Richardson, D.;
C.M.
Nature 399, 323-329, 1999
A:Title: Evidence for lateral gene transfer between Archaea and Bacteria from genome seq
A:Reference number: A72200; MUID:99287316; PMID:10360571
A/Accession: E72268
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-463 <ARN>
A:Cross-references: GB:AE001786; GB:AE000512; NID:94981873; PIDN:AA036391.1; PID:9498187
A:Experimental source: strain MSB8
C:Genetics:
A:Gene: TM1317

Query Match 83.3%; Score 30; DB 2; Length 463;
Best Local Similarity 85.7%; Pred. No. 70;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 EKSRTGD 7
Db 308 EKSRTGD 314
|||||

RESULT 13
S49641
L-galactonolactone oxidase (EC 1.1.3.24) - yeast (Saccharomyces cerevisiae)
N:Alternative names: D-arabinono-1,4-lactone oxidase; protein YML086c
C:Species: Saccharomyces cerevisiae
C>Date: 13-Jan-1995 #sequence_revision 10-Feb-1995 #text_change 19-Apr-2002
C/Accession: S49641
R:Genies, S.; Bowman, S.
submitted to the EMBL Data Library, November 1994
A:Reference number: S49627
A/Accession: S49641
A:Molecule type: DNA
A:Residues: 1-526 <GEN>
A:Cross-references: EMBL:Z46660; NID:9575702; PID:9575717; MIPS:YML086c
R:Hu, W.K.; Kim, S.T.; Kim, J.Y.; Hwang, S.W.; Kang, S.O.
submitted to the EMBL Data Library, November 1995

A:Reference number: S61944
A/Accession: S61944
A:Molecule type: DNA
A:Residues: 1-526 <HU>
A:Cross-references: EMBL:U40390; NID:91103916; PID:91103917
A:Experimental source: strain ATCC 24858
C:Genetics:
A:Gene: SGD:ALO1; ALO
A:Cross-references: SGD:S0004551
A:Map position: 131
C:Keywords: ascorbic acid biosynthesis; oxidoreductase; transmembrane protein
F:172-188/Domain: transmembrane #status predicted <TM>

Query Match 83.3%; Score 30; DB 2; Length 526;
Best Local Similarity 85.7%; Pred. No. 80;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 EKSRTGD 7
Db 293 EKSRTGD 299
|||||

RESULT 14
H70441
ribosomal protein L15 - Aquifex aeolicus
C:Species: Aquifex aeolicus
C>Date: 08-May-1998 #sequence_revision 08-May-1998 #text_change 13-Aug-1999
C/Accession: H70441
R:Decker, G.; Warren, P.V.; Gaasterland, T.; Young, W.G.; Lenox, A.L.; Graham, D.E.;
V.
Nature 392, 353-358, 1998
A:Title: The complete genome of the hyperthermophilic bacterium Aquifex aeolicus.
A:Reference number: A70300; MUID:98196666; PMID:9537320
A/Accession: H70441
A>Status: preliminary; nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-149 <AQ>
A:Cross-references: GB:AE000749; NID:92983975; PIDN:AA07532.1; PID:92983986; GB:AE00
A:Experimental source: strain VF5
C:Genetics:
A:Gene: rplO
C:Superfamily: Escherichia coli ribosomal protein L15

Query Match 80.6%; Score 29; DB 2; Length 149;
Best Local Similarity 71.4%; Pred. No. 35;
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

OY 1 EKSRTGD 7
Db 39 QRSRTGD 45
|||||

RESULT 15
E95307
hypothetical protein Sma0689 [imported] - Sinorhizobium meliloti (strain 1021) megapl
C:Species: Sinorhizobium meliloti
C>Date: 24-Aug-2001 #sequence_revision 24-Aug-2001 #text_change 30-Sep-2001
C/Accession: E95307
R:Barnett, M.J.; Fisher, R.P.; Jones, T.; Komp, C.; Abola, A.P.; Barloy-Hubler, F.; B
poc. Natl. Acad. Sci. U.S.A. 98, 9883-9888, 2001
A:Title: Nucleotide sequence and predicted functions of the entire Sinorhizobium mell
A:Reference number: A95262; MUID:21396509; PMID:11481432
A/Accession: E95307
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-316 <KUR>
A:Cross-references: GB:AE006469; PIDN:AAK65023.1; PID:914523453; GSPDB:GN00165
A:Experimental source: Strain 1021, megaplasmid psymk
R:Gallbert, F.; Finan, T.M.; Long, S.R.; Puhler, A.; Abola, P.; Ampe, F.; Barloy-Hubl
pela, D.; Chalm, P.; Cowie, A.; Davis, R.W.; Dreano, S.; Federspiel, N.A.; Fisher, R.
L.; Hyman, R.W.; Jones, T.
science 293, 668-672, 2001

A:Authors: Kahn, D.; Kahn, M.L.; Kalman, S.; Keating, D.H.; Kiss, E.; Komp, C.; Lelaure,
hehault, P.; Vandenbol, M.; Vorholter, F.J.; Weidner, S.; Wells, D.H.; Wong, K.; Yen, K.
A:Title: The composite genome of the legume symbiont *Sinorhizobium meliloti*.
A:Reference number: A96039; KUID:21368234; PMID:11474104
A:Contents: annotation
C:Genetics:
A:Gene: Sma0689
A:Genome: plasmid

Query Match 80.6%; Score 29; DB 2; length 316;
Best local Similarity 71.4%; Pred. No. 79;
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
Qy 1 EKSRTGD 7
|||:
DB 221 EKARTGE 227

Search completed: November 12, 2002, 17:01:02
Job time : 2.08155 secs

GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on: November 12, 2002, 16:49:26 : Search time 0.600858 Seconds
(Without alignments)
483.199 Million cell updates/sec

Title: US-09-848-271-2_COPY_105_111
Perfect score: 36
Sequence: 1 EKSRTGD 7

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 112892 seqs, 41476328 residues

Total number of hits satisfying chosen parameters: 112892

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SwissProt_40:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match Length	ID	Description
1	36	100.0	1 TR17_HUMAN	Q02223 homo sapien
2	32	88.9	1 RPOD_PEA	P12227 pismu sativ
3	32	88.9	1 RPOD_SPIOL	P11704 spindacta ol
4	32	88.9	1 RPOD_ARATH	P56764 arabidopsis
5	32	88.9	1 RPOD_SINLA	O9thv5 sinapis alb
6	32	88.9	1 RPOD_TOBAC	P38550 nicotiana t
7	30	83.3	1 ALO_YEAST	P54783 saccharomyc
8	30	83.3	1 RPOD_GUTR	O78483 guillardia
9	29	80.6	1 RIL5_MOUSE	O67561 aquifex aeo
10	29	80.6	1 RPOD_MESVI	O9mus7 mesostigma
11	29	80.6	1 RPOD_YEAST	P13443 saccharomyc
12	28	77.8	1 GLN1_METTH	O26758 methanobact
13	28	77.8	1 YCW1_YEAST	P25642 saccharomyc
14	28	77.8	1 YS98_MYCTU	Q10819 mycobacteri
15	28	77.8	1 TSD2_STRPN	P09357 streptococc
16	28	77.8	1 PIX1_XENLA	O9w751 xenopus lae
17	28	77.8	1 CYR_GUTR	O78484 guillardia
18	28	77.8	1 HYPE_BRAJA	P31906 bradyrhizob
19	28	77.8	1 IDH2_KLULA	O94230 kluyveromyc
20	28	77.8	1 ALG1_PSEBY	O91172 pseudomonas
21	28	77.8	1 YDEU_ECOLI	P77266 escherichia
22	28	77.8	1 MANC_ECO57	O85342 escherichia
23	28	77.8	1 SPI5_STRGR	P19471 streptomyce
24	28	77.8	1 MDIA_BUCAI	P57551 buchnera ap
25	28	77.8	1 AFAM_RAT	P36953 rattus norv
26	28	77.8	1 AFAM_MOUSE	O89020 mus musculu
27	28	77.8	1 Z143_HUMAN	P27474 homo sapien
28	28	77.8	1 COPA_ENTHR	P21113 enterococcu
29	28	77.8	1 UVRG_STRCO	O92512 streptomyce
30	28	77.8	1 ITA1_HUMAN	P56193 homo sapien
31	28	77.8	1 ITA1_RAT	P18614 rattus norv
32	27	75.0	1 IF5A_PYRAE	P56655 pyrobaculum
33	27	75.0	1 RL15_HAEIN	P44353 haemophilus

34	27	75.0	1 Y5G7_CLOAB	P23672 clostridium
35	27	75.0	1 U6X2_YEAST	P32772 saccharomyc
36	27	75.0	1 CP22_COL6L	O00371 colibacteric
37	27	75.0	1 YIHL_ECOLI	P32133 escherichia
38	27	75.0	1 YPBE_BACSU	P50731 bacillus su
39	27	75.0	1 SUBB_SYNY3	P74158 synochocyst
40	27	75.0	1 AIGL_AZOVI	O52195 azotobacter
41	27	75.0	1 GAFR_MOUSE	P23336 mus musculu
42	27	75.0	1 YCF1_MESVI	O9mun0 mesostigma
43	27	75.0	1 SECY_BUCAI	O6491 aquifex aeo
44	27	75.0	1 SECY_BUCAI	P57571 buchnera ap
45	27	75.0	1 LAMB_ECO57	O8x5w7 escherichia

ALIGNMENTS

RESULT 1	ID	TR17_HUMAN	STANDARD	PRT: 184 AA.
AC	Q02223			
DT	01-JUL-1993	(Rel. 26, Created)		
DT	01-JUL-1993	(Rel. 26, Last sequence update)		
DT	15-JUN-2002	(Rel. 41, Last annotation update)		
DE	Tumor necrosis factor receptor superfamily member 17 (B-cell maturation protein).			
GN	TNFRSF17 OR BCM4 OR BCM.			
OS	Homo sapiens (human).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.			
OX	NCBI_TaxID=9606;			
RN	[1]			
RP	SEQUENCE FROM N.A., AND CHROMOSOMAL TRANSLOCATION.			
RC	TISSUE=peripheral blood leukocytes, and Lymph node;			
RX	MEDLINE=33010984; PubMed=1396583;			
RA	Laabl Y., Gras M.P., Carbonnel F., Brovet J.C., Berger R.,			
RA	Larsen C.J., Tsapis A.;			
RT	"A new gene, BCM, on chromosome 16 is fused to the interleukin 2 gene by a t(4;16)(q26;p13) translocation in a malignant T cell lymphoma.";			
RT	EMBO J. 11:3897-3904(1992).			
RL	[2]			
RP	SEQUENCE FROM N.A.			
RX	MEDLINE=94218235; PubMed=8165126;			
RA	Laabl Y., Gras M.P., Brovet J.C., Berger R., Larsen C.J., Tsapis A.;			
RT	"The BCM gene, preferentially expressed during B lymphoid maturation, is bidirectionally transcribed.";			
RL	Nucleic Acids Res. 22:1147-1154(1994).			
RN	[3]			
RP	SEQUENCE FROM N.A.			
RX	MEDLINE=99425270; PubMed=10493829;			
RA	Loftus B.J., Kim U.-J., Sneddon V.P., Kalush F., Brandon R.,			
RA	Fuhrmann J., Mason T., Crosby M.L., Barnstead M., Cronin L.,			
RA	Deslats Mays A., Cao Y., Xu R.X., Kang H.-L., Mitchell S.,			
RA	Eichler E.E., Harris P.C., Venter J.C., Adams M.D.;			
RT	"Genome duplications and other features in 12 Mb of DNA sequence from human chromosome 16p and 16q.";			
RL	Genomics 60:295-308(1999).			
RN	[4]			
RP	SEQUENCE FROM N.A., AND VARIANT THR-153.			
RX	MEDLINE=21419161; PubMed=11528522;			
RA	Kawasaki A., Tsuchiya N., Fukazawa T., Hashimoto H., Tokunaga K.;			
RT	"Presence of four major haplotypes in human BCM4 gene: lack of association with systemic lupus erythematosus and rheumatoid arthritis.";			
RL	Genes Immun. 2:276-279(2001).			
RN	[5]			
RP	FUNCTION.			
RX	MEDLINE=20363816; PubMed=10903733;			
RA	Hatzoglou A., Rousset J., Bourgeade M.-F., Rogier E., Madry C.,			
RA	Inoue J., Devergne O., Tsapis A.;			
RT	"TNF receptor family member BCM4 (B cell maturation) associates with TNF receptor-associated factor (TRAF) 1, TRAF2, and TRAF3 and activates NF-kappa B, elk-1, c-Jun N-terminal kinase, and p38			

RT mitogen-activated protein kinase.";
 RL Immunol. 165:1322-1330(2000).
 [6]
 RA FUNCTION.
 RP MEDLINE-20259066; PubMed-10801128;
 RA Gross J.A., Johnston J., Mudri S., Enselman R., Dillon S.R.,
 Madden K., Xu W., Parrish-Novak J., Foster D., Lofton-Day C.,
 Moore M., Littau A., Grossman A., Haugen H., Foley K., Blumberg H.,
 RA Harrison K., Kindsvogel W., Clegg C.H.;
 RT "TACI and BCMA are receptors for a TNF homologue implicated in B-cell
 autoimmune disease.";
 RL Nature 404:995-999(2000).
 [7]
 RP FUNCTION, AND INTERACTION WITH APRIL AND BAFF.
 RX MEDLINE-21170294; PubMed-10973284;
 RA Yu G., Boone T., Delaney J., Hawkins N., Kelley M., Ramakrishnan M.,
 McCabe S., Qiu W.R., Kornuc M., Xia X.-Z., Guo J., Stollina M.,
 RA Boyle W.J., Sarsori I., Han H., Senaldi G., Thellier L.E.;
 RT "APRIL and TALL-1 and receptors BCMA and TACI: system for regulating
 humoral immunity.";
 RL Nat. Immunol. 1:252-256(2000).
 [8]
 RP INTERACTION WITH TRAF5 AND TRAF6.
 RX MEDLINE-20381353; PubMed-10908663;
 RA Shu H.-B., Johnson H.;
 RT "B cell maturation protein is a receptor for the tumor necrosis factor
 family member TALL-1.";
 RL Proc. Natl. Acad. Sci. U.S.A. 97:9156-9161(2000).
 CC -1- FUNCTION: Receptor for TNFSF18/BLyS/BAFF and TNFSF13/APRIL.
 CC Promotes B-cell survival and plays a role in the regulation of
 CC humoral immunity. Activates NF-kappa-B and JNK.
 CC -1- SUBUNIT: Associates with TRAF1, TRAF2, TRAF3, TRAF5 and TRAF6.
 CC and perinuclear Golgi-like structures.
 CC -1- TISSUE SPECIFICITY: Expressed in mature B-cells, but not in T-
 CC cells or monocytes.
 CC -1- DISEASE: A FORM OF T-CELL ACUTE LYMPHOBLASTIC LEUKEMIA (T-ALL) IS
 CC CHARACTERIZED BY A CHROMOSOMAL TRANSLOCATION T(4;16)(Q26;P13)
 CC WHICH INVOLVES BCMA AND IL2.
 CC -1- SIMILARITY: CONTAINS 1 TNFR-CYS REPEAT.
 CC -----
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 CC -----
 DR EMBL: Z14954; CAAT78679.1; -
 DR EMBL: Z29575; CAAB2691.1; -
 DR EMBL: Z29574; CAAB2690.1; -
 DR EMBL: U95742; AAB67251.1; -
 DR EMBL: AB052772; BAB60895.1; -
 DR PIR: S31208; S31208.
 DR PIR: S31209; S31209.
 DR Genew: HGNC:11913; TNFRSF17.
 DR MIM: 109545; -
 KW Receptor: Immune response: Proto-oncogene: Signal-anchor:
 KW Transmembrane: Chromosomal translocation: polymorphism.
 KW DOMAIN 1 54 EXTRACELLULAR (POTENTIAL).
 FT DOMAIN 53 77 SIGNAL-ANCHOR (TYPE III MEMBRANE PROTEIN)
 FT TRANSMEM 53 77 CYTOPLASMIC (POTENTIAL).
 FT DOMAIN 78 184
 FT REPEAT 7 41 TNFR-CYS.
 FT SITE 3 4 BREAKPOINT FOR TRANSLOCATION TO FORM
 FT DISURFID 8 21 INTERLEUKIN 2/BGM ONCOGENE.
 FT DISURFID 24 37 BY SIMILARITY.
 FT DISURFID 28 41 BY SIMILARITY.
 FT VARIANT 153 153 A -> T.
 FT SEQUENCE 184 AA: 20138 MW: 277AF11E2767D932 CRC64;
 SQ

Query Match 100.0%; Score 36; DB 1; Length 184;
 Best Local Similarity 100.0%; Pred. No. 0.32;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 EKSRTGD 7
 Db 105 EKSRTGD 111
 RESULT 2
 RPOD_PEA
 ID RPOD_PEA STANDARD; PRT; 1163 AA.
 AC P12227;
 DT 01-OCT-1989 (Rel. 12, Created)
 DT 01-OCT-1989 (Rel. 12, Last sequence update)
 DT 01-JUL-1993 (Rel. 26, Last annotation update)
 DE DNA-directed RNA polymerase beta" chain (EC 2.7.7.6) (Fragment).
 GN RPOC2.
 OS Pisum sativum (Garden pea).
 OC Chloroplast.
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
 OC Oxysiphonales; Fabales; Fabaceae; Papilionoideae; Viciae; Pisum.
 OX NCBI_TaxID:3888;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE-86323089; PubMed-3530249;
 RA Cozens A.L., Walker J.E.;
 RT "Pea chloroplast DNA encodes homologues of Escherichia coli ribosomal
 RT subunit S2 and the beta'-subunit of RNA polymerase.";
 RL Biochem. J. 236:453-460(1986).
 CC -1- FUNCTION: DNA-DEPENDENT RNA POLYMERASE CATALYZES THE TRANSCRIPTION
 CC OF DNA INTO RNA USING THE FOUR RIBONUCLEOSIDE TRIPHOSPHATES AS
 CC SUBSTRATES.
 CC -1- CATALYTIC ACTIVITY: N nucleoside triphosphate - N diphosphate +
 CC (RNA)(N).
 CC -1- SUBUNIT: IN CHLOROPLAST THE RNA POLYMERASE IS COMPOSED OF FOUR
 CC SUBUNITS: ALPHA, BETA', AND BETA".
 CC -----
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 CC -----
 DR EMBL: X03912; CAAT7545.1; -
 DR PIR: S07137; S07137.
 DR InterPro: IPR002879; RNA_pol_A2.
 DR Pfam: PF01854; RNA_pol_A2; 2.
 KM Transferrin; Transcription; DNA-directed RNA polymerase; Chloroplast.
 FT NON_TER 1
 FT SEQUENCE 1163 AA: 133598 MW: C92E7BE0A3FDB525 CRC64;
 SO
 Query Match 88.9%; Score 32; DB 1; Length 1163;
 Best Local Similarity 85.7%; Pred. No. 32;
 Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 QY 1 EKSRTGD 7
 Db 924 EKSRTGD 930
 RESULT 3
 RPOD_SPIOL
 ID RPOD_SPIOL STANDARD; PRT; 1361 AA.
 AC P11704;
 DT 01-OCT-1989 (Rel. 12, Created)
 DT 01-OCT-1989 (Rel. 12, Last sequence update)
 DT 01-OCT-2001 (Rel. 40, Last annotation update)
 DE DNA-directed RNA polymerase beta" chain (EC 2.7.7.6).
 DE

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GN RPOC2.
OS Spinacia oleracea (Spinach).
OC Chloroplast.
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
OC Caryophyllales; Caryophyllales; Chenopodiaceae; Spinacia.
OX NCBI_TaxID=3562;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=88316931; PubMed=3045324;
RA Hudson G.S., Holton T.A., Whitefield P.R., Bottomley W.;
RT "Spinach chloroplast rpoBc genes encode three subunits of the
RT chloroplast RNA polymerase.";
RL J. Mol. Biol. 200; 639-654(1988).
RN [2]
RP SEQUENCE FROM N.A.
RX STRAIN=cv. Geant d'hiwer, and cv. Monatol;
RT MEDLINE=21187424; PubMed=11292076;
RA Schmitz-Linneweber C., Maier R.M., Alcaraz J.-P., Cottet A.,
RA Herrmann R.G., Maché R.;
RT "The plastid chromosome of spinach (Spinacia oleracea): complete
RT nucleotide sequence and gene organization.";
RL Plant Mol. Biol. 45:307-315(2001).
CC -1- FUNCTION: DNA-DEPENDENT RNA POLYMERASE CATALYZES THE TRANSCRIPTION
CC OF DNA INTO RNA USING THE FOUR RIBONUCLEOSIDE TRIPHOSPHATES AS
CC SUBSTRATES.
CC -1- CATALYTIC ACTIVITY: N nucleoside triphosphate - N diphosphate +
CC (RNA)(N).
CC -1- SUBUNIT: IN CHLOROPLAST THE RNA POLYMERASE IS COMPOSED OF FOUR
CC SUBUNITS: ALPHA, BETA, BETA', AND BETA".
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-----
DR EMBL: AJ400848; CAB8715.1; -.
DR PIR: A29959; A29959.
DR HSSP: O9KRW6; IHOM.
DR InterPro: IPR000722; RNA_pol_A.
DR InterPro: IPR002879; RNA_pol_A2.
DR Pfam: PF00623; RNA_pol_A; 1.
DR Pfam: PF01854; RNA_pol_A2; 2.
DR Transferrase; Transcription; DNA-directed RNA polymerase; Chloroplast.
KM SEQUENCE 1361 AA; 154768 MW; 19F8C42B81B17E8 CRC64;
SQ
Query Match 88.9%; Score 32; DB 1; Length 1361;
Best Local Similarity 85.7%; Pred. No. 38;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
OY 1 EKSRTGD 7
DB 1130 EKSRTGD 1129

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RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN=cv. Columbia;
RT MEDLINE=20039611; PubMed=10574454;
RA Sato S., Nakamura Y., Kaneko T., Asamizu E., Tabata S.;
RT "Complete structure of the chloroplast genome of Arabidopsis
RT thaliana.";
RL DNA Res. 6:283-290(1999).
CC -1- FUNCTION: DNA-DEPENDENT RNA POLYMERASE CATALYZES THE TRANSCRIPTION
CC OF DNA INTO RNA USING THE FOUR RIBONUCLEOSIDE TRIPHOSPHATES AS
CC SUBSTRATES.
CC -1- CATALYTIC ACTIVITY: N nucleoside triphosphate - N diphosphate +
CC (RNA)(N).
CC -1- SUBUNIT: IN CHLOROPLAST THE RNA POLYMERASE IS COMPOSED OF FOUR
CC SUBUNITS: ALPHA, BETA, BETA', AND BETA".
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-----
DR EMBL: AP000423; BAB84375.1; -.
DR HSSP: O9KRW6; IHOM.
DR InterPro: IPR000722; RNA_pol_A.
DR InterPro: IPR002879; RNA_pol_A2.
DR Pfam: PF00623; RNA_pol_A; 1.
DR Pfam: PF01854; RNA_pol_A2; 2.
DR Transferrase; Transcription; DNA-directed RNA polymerase; Chloroplast.
KM SEQUENCE 1376 AA; 156365 MW; 7CBB5820163E2B9D CRC64;
SQ
Query Match 88.9%; Score 32; DB 1; Length 1376;
Best Local Similarity 85.7%; Pred. No. 39;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
OY 1 EKSRTGD 7
DB 1130 EKSRTGD 1136

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RESULT 4
RPOD_ARATH STANDARD; PRT: 1376 AA.
AC P56764;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE DNA-directed RNA polymerase beta" chain (EC 2.7.7.6).
GN RPOC2.
OS Arabidopsis thaliana (Mouse-ear cress).
OC Chloroplast.
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eurosids II; Brassicales; Brassicaceae; Arabidopsis.
OX NCBI_TaxID=3702;

```

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RESULT 5
RPOD_SINAPL STANDARD; PRT: 1384 AA.
AC O9THV5;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE DNA-directed RNA polymerase beta" chain (EC 2.7.7.6).
GN RPOC2.
OS Sinapis alba (white mustard) (Brassica hirta).
OC Chloroplast.
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eurosids II; Brassicales; Brassicaceae; Sinapis.
OX NCBI_TaxID=3728;
RN [1]
RP SEQUENCE FROM N.A. AND SEQUENCE OF 6-20.
RX STRAIN=cv. Albalros; TISSUE=Cotyledon;
RT MEDLINE=20059369; PubMed=10601874;
RA Pfannschmidt T., Ogrzewalla K., Baginsky S., Sickmann A., Meyer H.E.,
RA Link G.;
RT "The multisubunit chloroplast RNA polymerase A from mustard (Sinapis
RT alba L.). Integration of a prokaryotic core into a larger complex
RT with organelle-specific functions.";
RL Eur. J. Biochem. 267:253-261(2000).
CC -1- FUNCTION: DNA-DEPENDENT RNA POLYMERASE CATALYZES THE TRANSCRIPTION
CC OF DNA INTO RNA USING THE FOUR RIBONUCLEOSIDE TRIPHOSPHATES AS
CC SUBSTRATES.
CC -1- CATALYTIC ACTIVITY: N nucleoside triphosphate - N diphosphate +
CC (RNA)(N).
CC -1- SUBUNIT: IN CHLOROPLAST THE RNA POLYMERASE IS COMPOSED OF FOUR

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CC SUBUNITS: ALPHA, BETA, BETA', AND BETA'.
CC -----
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CC -----
CC EMBL: AJ243754; CAB48415.2; -.
CC DR HSSP: O9KM06; IHQM.
CC DR InterPro: IPR000722; RNA_pol_A.
CC DR InterPro: IPR002879; RNA_pol_A2.
CC DR Pfam: PF00623; RNA_pol_A; 1.
CC DR Pfam: PF01854; RNA_pol_A2; 1.
CC DR Transferase: Transcription; DNA-directed RNA polymerase; Chloroplast.
CC SEQUENCE 1384 AA; 157740 MW; 9A7BAD02053F4A80 CRC64;

Query Match 88.9%; Score 32; DB 1; Length 1384;
Best Local Similarity 85.7%; Pred. No. 39;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 EKSRTGD 7
DB 1138 EKSRSKD 1144

RESULT 6
PROD_TOBAC STANDARD; PRT: 1388 AA.
AC P38550;
ID RPOD_TOBAC
DR 01-OCT-1994 (Rel. 30, Created)
DT 01-OCT-1994 (Rel. 30, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE DNA-directed RNA polymerase beta* chain (EC 2.7.7.6).
GN Nicotiana tabacum (Common tobacco).
OS Chloroplast.
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
OC Asteridae; easterids I; Solanales; Solanaceae; Nicotiana.
OX NCBI_TaxID=4097;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=cv. Bright Yellow 4;
RA Shinozaki K., Ohme M., Tanaka M., Wakasugi T., Hayashida N.,
RA Matsubayashi T., Zaita N., Chunwongse J., Obokata J.,
RA Yamaguchi-Shinozaki K., Ohno C., Torazawa K., Meng B.-Y., Sugita M.,
RA Deno H., Kamogashira T., Yamada K., Kusuda J., Takaiwa F., Kato A.,
RA Tomoh N., Shimada H., Sugiyama M.;
RT "The complete nucleotide sequence of the tobacco chloroplast genome:
RT its gene organization and expression.";
RT EMBL J. 5:2043-2049(1986).
RN [2]
RP MEDLINE=94003079; PubMed=8400137;
RA Olmstead R.G., Sweere J.A., Wolfe K.H.;
RT "Nucleic extra nucleotide in ndh gene of tobacco chloroplast DNA: a
RT summary of revisions to the 1986 genome sequence.";
RN Plant Mol. Biol. 22:1191-1193(1993).
CC -1- FUNCTION: DNA-DEPENDENT RNA POLYMERASE CATALYZES THE TRANSCRIPTION
CC OF DNA INTO RNA USING THE FOUR RIBONUCLEOSIDE TRIPHOSPHATES AS
CC SUBSTRATES.
CC -1- CATALYTIC ACTIVITY: N nucleoside triphosphate = N diphosphate +
CC (RNA)(N).
CC -1- SUBUNIT: IN CHLOROPLAST THE RNA POLYMERASE IS COMPOSED OF FOUR
CC SUBUNITS: ALPHA, BETA, BETA', AND BETA".
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL: 200044; CA77410.1; ALT_SEQ.
CC DR HSSP: O9KM06; IHQM.
CC DR InterPro: IPR000722; RNA_pol_A.
CC DR InterPro: IPR002879; RNA_pol_A2.
CC DR Pfam: PF00623; RNA_pol_A; 1.
CC DR Pfam: PF01854; RNA_pol_A2; 2.
CC DR Transferase: Transcription; DNA-directed RNA polymerase; Chloroplast.
CC SEQUENCE 1388 AA; 156840 MW; 41FD7F238913186C CRC64;

Query Match 88.9%; Score 32; DB 1; Length 1388;
Best Local Similarity 85.7%; Pred. No. 39;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 EKSRTGD 7
DB 1135 EKSRSKD 1141

RESULT 7
ALO_YEAST STANDARD; PRT: 526 AA.
AC P54783; Q42618;
ID ALO_YEAST
DR 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE D-arabinono-1,4-lactone oxidase (EC 1.1.3.37) (ALO) (L-galactono-
DE gamma-lactone oxidase).
GN ALO1 OR YML086C.
OS Saccharomyces cerevisiae (Baker's yeast).
OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
OC Saccharomycetales; Saccharomycetaceae; Saccharomyces.
OX NCBI_TaxID=4932;
RN [1]
RP SEQUENCE FROM N.A. AND SEQUENCE OF 86-105 AND 349-363.
RC STRAIN=ATCC 24858 / WH101;
RX MEDLINE=99140446; PubMed=10094636;
RA Huh W.-K., Lee B.-H., Kim S.-T., Kim Y.-R., Rhie G.-E., Baek Y.-W.,
RA Hwang C.-S., Lee J.-S., Kang S.-O.;
RT "D-Erythraascorbic acid is an important antioxidant molecule in
RT Saccharomyces cerevisiae.";
RN Mol. Microbiol. 30:895-903(1998).
RN [2]
RP SEQUENCE FROM N.A.
RA Nishikimi M., Ohta Y., Ishikawa T.;
RT "Identification of the yeast genomic sequence encoding L-galactono-
RT gamma-lactone oxidase.";
RN Submitted (DEC-1997) to the EMBL/Genbank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN=S288c / AB972;
RA Gentles S., Bowman S., Barrell B.G., Rajandream M.A.;
RT Submitted (NOV-1994) to the EMBL/Genbank/DBJ databases.
CC -1- FUNCTION: CAN OXIDIZE L-GULOONO-1,4-LACTONE AS WELL AS D-ARABINONO-
CC 1,4-LACTONE AND L-GALACTONO-1,4-LACTONE.
CC -1- CATALYTIC ACTIVITY: D-arabinono-1,4-lactone + O(2) = D-erythro-
CC ascorbate + H(2)O(2).
CC -1- COFACTOR: FAD.
CC -1- PATHWAY: D-erythraascorbic acid biosynthesis; final step.
CC -1- SUBCELLULAR LOCATION: Mitochondrial. Membrane-embedded.
CC -1- SIMILARITY: Belongs to the oxygen-dependent FAD-linked
CC oxidoreductase family.
CC -----
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CC      -----
DR      EMBL: U40390; AAC98538.1; -.
DR      EMBL: AB009401; BAA23804.1; -.
DR      EMBL: Z46660; CA86652.1; -.
DR      SGD: S0004551; AL01.
DR      InterPro: IPR001575; Oxid.FAD_Bind.
DR      Pfam: PF01565; FAD_binding_4; 1.
DR      Prosite: PS00862; OX2_COVAL_FAD; 1.
DR      Oxidoreductase; Flavoprotein; FAD; Mitochondrion; Membrane.
FT      BINDING 36 36
FT      CONFLICT 417 417 A -> P (IN REF. 2).
SQ      SEQUENCE 526 AA; 59493 MW; 942177A7A738EC8 CRC64;

Query Match      83.3%; Score 30; DB 1; Length 526;
Best Local Similarity 85.7%; Pred. No. 38;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY      1 EKSRTGD 7
Db      293 EKSRTGD 299

RESULT 8
RPD_GUTH      STANDARD; PRT; 1286 AA.
AC      078483;
DT      15-DEC-1998 (Rel. 37, Created)
DT      15-DEC-1998 (Rel. 37, Last sequence update)
DT      15-JUL-1999 (Rel. 38, Last annotation update)
DE      DNA-directed RNA polymerase beta" chain (EC 2.7.7.6).
GN      RPOC2.
OS      Galliardia theta (Cryptomonas phi).
OC      Chloroplast.
OC      Eukaryota; Cryptophyta; Cryptomonadaceae; Galliardia.
OX      NCBI_TaxID=55529;
RN      [1]
RP      SEQUENCE FROM N.A.
RX      MEDLINE=99128221; PubMed=9929392;
RA      Douglas S.E., Penny S.L.;
RT      *The plastid genome of the cryptophyte alga, Galliardia theta:
RT      complete sequence and conserved syntenic groups confirm its common
RT      ancestry with red algae.
RL      J. Mol. Evol. 48:236-244(1999).
CC      -1- FUNCTION: DNA-DEPENDENT RNA POLYMERASE CATALYZES THE TRANSCRIPTION
CC      OF DNA INTO RNA USING THE FOUR RIBONUCLEOSIDE TRIPHOSPHATES AS
CC      SUBSTRATES.
CC      -1- CATALYTIC ACTIVITY: N nucleoside triphosphate - N diphosphate +
CC      (RNA)(n).
CC      -1- SUBUNIT: IN CHLOROPLAST THE RNA POLYMERASE IS COMPOSED OF FOUR
CC      SUBUNITS: ALPHA, BETA, BETA', AND BETA".
CC      -----
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CC      -----
DR      EMBL: AF041468; AAC35674.1; -.
DR      HSSP: Q9KM06; 1HQM.
DR      InterPro: IPR000722; RNA_POL_A.
DR      InterPro: IPR002879; RNA_POL_A2.
DR      Pfam: PF00623; RNA_POL_A; 1.
DR      Pfam: PF01854; RNA_POL_A2; 2.
DR      Transcription; DNA-directed RNA polymerase; Chloroplast.
KW      TRANSFERASE; RNA_POL_A2; 2.
SQ      SEQUENCE 1286 AA; 14504 MW; BEFF46FEFF5522C73 CRC64;

Query Match      83.3%; Score 30; DB 1; Length 1286;
Best Local Similarity 71.4%; Pred. No. 16+02;
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

OY      1 EKSRTGD 7
Db      39 QKSRSGD 45

RESULT 10
RPD_MESVI      STANDARD; PRT; 1223 AA.
AC      09M057;
DT      15-OCT-2001 (Rel. 40, Created)
DT      15-OCT-2001 (Rel. 40, Last sequence update)
DT      16-OCT-2001 (Rel. 40, Last annotation update)
DE      DNA-directed RNA polymerase beta" chain (EC 2.7.7.6).
GN      RPOC2.
OS      Mesostigma viride.
OC      Chloroplast.
OC      Eukaryota; Viridiplantae; Streptophyta; Mesostigmatoxiphyceae;
OC      Mesostigmatales; Mesostigmataceae; Mesostigma.
OX      NCBI_TaxID=41882;
RN      [1]

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RP SEQUENCE FROM N.A.
RC STRAIN-NIES-296;
RX MEDLINE=20150907; PubMed=10688199;
RT Lemieux C., Oltis C., Turmel M.;
RT "Ancestral chloroplast genome in Mesostigma viride reveals an early
RT branch of green plant evolution.";
RL Nature 403:649-652(2000).
CC -1- FUNCTION: DNA-DEPENDENT RNA POLYMERASE CATALYZES THE TRANSCRIPTION
CC OF DNA INTO RNA USING THE FOUR RIBONUCLEOSIDE TRIPHOSPHATES AS
CC SUBSTRATES.
CC -1- CATALYTIC ACTIVITY: N nucleoside triphosphate = N diphosphate +
CC (RNA)(N).
CC -1- SUBUNIT: IN CHLOROPLAST THE RNA POLYMERASE IS COMPOSED OF FOUR
CC SUBUNITS: ALPHA, BETA, BETA', AND BETA".
CC -----
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CC -----
DR EMBL: AF166114; AAF43824.1; -.
DR HSSP: Q9KMU6; 1HQM.
DR InterPro: IPR000722; RNA_POL_A.
DR InterPro: IPR002879; RNA_POL_A2.
DR Pfam: PF006623; RNA_POL_A2.1.
DR Pfam: PF01854; RNA_POL_A2.2.
DR Transferrase; Transcription; DNA-directed RNA polymerase; Chloroplast.
SQ SEQUENCE 1223 AA; 138048 MW; 4044E90805FC472A CRC64;

Query Match      80.6%; Score 29; DB 1; Length 1223;
Best Local Similarity 71.4%; Pred. No. 1.6e+02;
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 EKSRTGD 7
   1:1:111
Db 987 EQSKTGD 993

RESULT 11
RPOM YEAST
ID RPOM_YEAST STANDARD: PRT; 1351 AA.
AC P13433;
DT 01-JAN-1990 (Rel. 13, Created)
DT 01-JAN-1990 (Rel. 13, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE DNA-directed RNA polymerase, mitochondrial precursor (EC 2.7.7.6).
GN RPO41 OR YFL036W.
OS Saccharomyces cerevisiae (Baker's yeast).
OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
OC Saccharomycetales; Saccharomycetaceae; Saccharomycetes.
OX NCBI_TaxID=4932;
RN (1)
RP SEQUENCE FROM N.A.
RX MEDLINE=88002333; PubMed=3308116;
RT Masters B.S., Stohl L.L., Clayton D.A.;
RT "Yeast mitochondrial RNA polymerase is homologous to those encoded by
RT bacteriophages T3 and T7.";
RL Cell 51:89-99(1987).
RN (12)
RP SEQUENCE FROM N.A.
RC STRAIN-S288c / AB972;
RX MEDLINE=95400292; PubMed=7670463;
RA Murkaml Y., Naltou M., Haglwaara H., Shibata T., Ozawa M.,
RA Sasahana S.-I., Sasahana M., Tsuchiya Y., Soeda E., Yokoyama K.,
RA Yamazaki M., Tashiro H., Eki T.;
RT "Analysis of the nucleotide sequence of chromosome VI from
RT Saccharomyces cerevisiae.";
RL Nat. Genet. 10:261-268(1995).
CC -1- FUNCTION: DNA-DEPENDENT RNA POLYMERASE CATALYZES THE TRANSCRIPTION
CC OF DNA INTO RNA USING THE FOUR RIBONUCLEOSIDE TRIPHOSPHATES AS

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CC SUBSTRATES.
CC -1- CATALYTIC ACTIVITY: N nucleoside triphosphate = N diphosphate +
CC (RNA)(N).
CC -1- SUBCELLULAR LOCATION: Mitochondrial.
CC -1- SIMILARITY: BELONGS TO THE PHAGE AND MITOCHONDRIAL RNA POLYMERASES
CC FAMILY.
CC -----
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CC -----
DR EMBL: M17539; AAA35007.1; -.
DR EMBL: D50617; BAA09203.1; -.
DR PIR: A27336; A27336.
DR HSSP: P00573; IARO.
DR SGD: S0001858; RPO41.
DR InterPro: IPR002092; RNA_POL_phage.
DR Pfam: PF00940; RNA_POL_1.
DR PROSITE: PS00900; RNA_POL_PHAGE_1; 1.
DR PROSITE: PS00489; RNA_POL_PHAGE_2; 1.
KW Transferrase; DNA-directed RNA polymerase; Transcription;
KW Mitochondrion; Transil peptide.
FT TRANSIT 1
FT CHAIN 1 1351
FT ACT_SITE 945 945
FT ACT_SITE 1014 1014
FT ACT_SITE 1189 1189
FT CONFLICT 485 485
FT CONFLICT 900 901
FT SEQUENCE 1351 AA; 153080 MW; 505CB8CEB35666 CRC64;

Query Match      80.6%; Score 29; DB 1; Length 1351;
Best Local Similarity 85.7%; Pred. No. 1.8e+02;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 EKSRTGD 7
   1:1:111
Db 899 EKSRTGD 905

RESULT 12
GLNL_METH
ID GLNL_METH STANDARD: PRT; 115 AA.
AC O26758;
DT 15-JUL-1998 (Rel. 36, Created)
DT 15-JUL-1998 (Rel. 36, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Nitrogen regulatory protein P-II 1.
GN MTH662.
OS Methanobacterium thermoautotrophicum.
OC Archaea; Euryarchaeota; Methanobacteria; Methanobacteriales;
OC Methanobacteriaceae; Methanothermobacter.
OX NCBI_TaxID=187420;
RN (1)
RP SEQUENCE FROM N.A.
RC STRAIN-Delta H;
RX MEDLINE=98037514; PubMed=9371463;
RA Smith D.R., Doucette-Stamm L.A., Delonghery C., Lee H.-M., Dubois J.,
RA Aldredge T., Bashirzadeh R., Blakely D., Cook R., Gilbert K.,
RA Harrison D., Hoang L., Keagle P., Lum W., Pothier B., Qiu D.,
RA Spadafora R., Vicare R., Wang Y., Wierzbowski J., Gibson R.,
RA Jivani N., Caruso A., Bush D., Safer H., Patwell D., Prabhakar S.,
RA McDougall S., Shimer G., Goyal A., Pietrowski S., Church G.M.,
RA Daniels C.J., Mao J.-I., Rice P., Noelling J., Reeve J.N.;
RT "Complete genome sequence of Methanobacterium thermoautotrophicum
RT deltaH: functional analysis and comparative genomics.";
RL J. Bacteriol. 179:7133-7155(1997).
CC -1- FUNCTION: COULD BE INVOLVED IN THE REGULATION OF NITROGEN
CC FIXATION.

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CC -1- SIMILARITY: BELONGS TO THE P(II) PROTEIN FAMILY.
CC -----
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CC -----
CC EMBL: AE000846; AAB85167.1; -.
CC DR HSSP: P05826; 2P11.
CC DR InterPro: IPR002187; P1I_glnb.
CC DR Pfam: PF00543; P-1I; 1.
CC DR PRINTS: PR00340; P1I_glnb.
CC DR PRODOM: PD001194; P1I_glnb; 1.
CC DR PROSITE: PS00638; P1I_Glnb_CTER; 1.
CC DR Transcription regulation; Nitrogen fixation; Complete proteome.
CC SEQUENCE 115 AA; 12904 MW; 4E77B0AE979BA53 CRC64;
CC -----
Query Match
Best Local Similarity 77.8%; Score 28; DB 1; Length 115;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
OY 1 EKSRTGD 7
DB 82 ENARTGD 88

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ID YS98_MTCU STANDARD: PRT: 128 AA.
AC Q10819;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Hypothetical protein RV2898C.
GN RV2898C OR MT2966 OR MTCY274.29C.
OS Mycobacterium tuberculosis.
OC Bacteria; Actinobacteria; Actinobacteria (class); Actinobacteridae;
OC Actinomycetales; Corynebacterineae; Mycobacteriaceae; Mycobacterium.
CC NCBI_Taxid=1773;
CC [1]
CC SEQUENCE FROM N.A.
CC STRAIN=H37RV;
CC MEDLINE=98295987; PubMed=9634230;
CC Cole S.T., Brosch R., Parkhill J., Garnier T., Churcher C., Harris D.,
CC Gordon S.V., Eigmeier K., Gas S., Barry C.E. III, Tekala F.,
CC Badcock K., Basham D., Brown D., Chillingworth T., Connor R.,
CC Davies R., Devlin K., Feltwell T., Gentles S., Hamlin N., Holroyd S.,
CC Hornsby T., Jagels K., Krogh A., Mclean J., Moule S., Murphy L.,
CC Oliver S., Osborne J., Quail M.A., Rajandream M.A., Rogers J.,
CC Rutter S., Seeger K., Skelton S., Squares S., Squares R.,
CC Stulton J.E., Taylor K., Whitehead S., Barrett B.G.,
CC RT Deciphering the biology of Mycobacterium tuberculosis from the
CC RT complete genome sequence."
CC RL Nature 393:537-544(1998).
CC [2]
CC SEQUENCE FROM N.A.
CC RC STRAIN=CDC 1551 / Oshkosh;
CC RA Fleischmann R.D., Alland D., Eisen J.A., Carpenter L., White O.,
CC RA Peterson J., Deboy R., Dodson R., Gwinn M.L., Haft D., Hickey E.,
CC RA Kolony J.F., Nelson W.C., Umayam L.A., Ermolaeva M.D., Salzberg S.L.,
CC RA Deichler A., Ulterback T., Weidman J., Khouri H., Gill J., Mikula A.,
CC RA Biswal W.;
CC RT "Whole genome comparison of Mycobacterium tuberculosis clinical and
CC RT laboratory strains."
CC RL Submitted (APR-2001) to the EMBL/Genbank/DBJ databases.
CC CC -1- SIMILARITY: BELONGS TO THE UPF0102 FAMILY.
CC -----
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CC -----
CC EMBL: Z74024; CAA98371.1; -.
CC DR EMBL: AE007119; AAK47292.1; ALT_INIT.
CC DR TIGR: MT2966; -.
CC DR TubercuList; RV2898C; -.
CC DR InterPro: IPR003509; UPF0102.
CC DR Pfam: PF02021; UPF0102; 1.
CC DR TIGRFAMs: TIGR00252; TIGR00252; 1.
CC DR Hypothetical protein; Complete proteome.
CC SEQUENCE 128 AA; 14223 MW; BBEB1657FE0AF571 CRC64;
CC -----
Query Match
Best Local Similarity 77.8%; Score 28; DB 1; Length 128;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
OY 2 KSRITGD 7
DB 61 KTRITGD 66

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RESULT 15
ID T2D2_STRPN STANDARD: PRT: 288 AA.
AC P09357;
DT 01-MAR-1989 (Rel. 10, Last sequence update)

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DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Type II restriction enzyme DpnII (EC 3.1.21.4) (Endonuclease DpnII)
GN (R.DpnII).
OS Streptococcus pneumoniae.
OC Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
OC Streptococcus.
OX NCBI_TaxID=1313;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=87002480; PubMed=3019562;
RA Lacks S.A., Manarelli B.M., Springhorn S.S., Greenberg B.;
RT "Genetic basis of the complementary DpnI and DpnII restriction
RT systems of S. pneumoniae: an intercellular cassette mechanism.";
RL Cell 46:993-1000(1986).
RN [2]
RP SEQUENCE OF 1-11.
RX MEDLINE=88062686; PubMed=2824782;
RA de la Campa A.G., Purushottam K., Springhorn S.S., Lacks S.A.;
RT "Proteins encoded by the DpnII restriction gene cassette. Two
RT methylases and an endonuclease.";
RL J. Mol. Biol. 196:457-469(1987).
CC -1- FUNCTION: RECOGNIZES THE DOUBLE-STRANDED UNMETHYLATED SEQUENCE
CC GATC AND CLEAVES BEFORE G-1.
CC -1- CATALYTIC ACTIVITY: Endonucleolytic cleavage of DNA to give
CC specific double-stranded fragments with terminal 5'-phosphates.
CC -1- SUBUNIT: HOMODIMER.
CC -1- SIMILARITY: TO R.MBOI AND R.LLAII.
CC -----
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CC -----
DR EMBL: M14339; AAA8582.1; -
DR PIR: B24372; B24372.
DR REBASE: 777; DpnII.
KW Hydrolase; Endonuclease; Nuclease; Restriction system.
SQ SEQUENCE 288 AA; 33585 MW; F7346EFA6940EB33 CRC64;

Query Match 77.88; Score 28; DB 1; Length 288;
Best Local Similarity 83.38; Pred. NO. 54;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY 2 KSRTGD 7
1:|||||
Db 144 KNRTGD 149

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Search completed: November 12, 2002, 16:58:59
 Job time : 1.60086 secs

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OM protein - protein search, using sw model

Run on: November 12, 2002, 16:56:16 ; Search time 2.13305 Seconds
(Without alignments)
676.183 Million cell updates/sec

Title: US-09-848-271-2_COPY_105_111

Perfect score: 36

Sequence: 1 EKSRTGD 7

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 671580 seqs, 206047115 residues

Total number of hits satisfying chosen parameters: 671580

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :
1: SP archaea:*
2: SP bacteria:*
3: SP fungi:*
4: SP human:*
5: SP invertebrate:*
6: SP mammal:*
7: SP mhc:*
8: SP organelle:*
9: SP phage:*
10: SP plant:*
11: SP rodent:*
12: SP virus:*
13: SP vertebrate:*
14: SP unclassified:*
15: SP virus:*
16: SP bacteriophage:*
17: SP archaea:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	91.7	585	16	007550	007550 bacillus su
2	88.9	868	16	08XL40	08XL40 clostridium
3	88.9	1118	5	09VD20	09VD20 drosophila
4	88.9	1186	5	0878S8	0878S8 drosophila
5	88.9	1332	8	09BHS7	09BHS7 lotus japon
6	88.9	1386	8	09WTM3	09WTM3 oenothera h
7	88.9	1389	10	08S8Y1	08S8Y1 atropa bell
8	86.1	132	2	09AG08	09AG08 wolbachia s
9	86.1	248	2	082969	082969 bacillus sp
10	86.1	281	10	08RMD7	08RMD7 arbidopsin
11	86.1	646	16	09VQ4	09VQ4 staphylococ
12	86.1	1195	10	09C730	09C730 arbidopsin
13	86.1	1246	10	09C609	09C609 arbidopsin
14	83.3	79	17	082TW7	082TW7 pyrobaculum
15	83.3	92	16	08UK19	08UK19 agrobacteri
16	83.3	160	16	097EE8	097EE8 clostridium

17	30	83.3	351	10	08RUB2	08RUB2 oryza sativ
18	30	83.3	362	12	091TF3	091TF3 oat mosaic
19	30	83.3	362	12	091TF2	091TF2 oat mosaic
20	30	83.3	396	16	08VAX2	08VAX2 bruceella me
21	30	83.3	439	5	0917X6	0917X6 drosophila
22	30	83.3	448	12	091BP9	091BP9 oat mosaic
23	30	83.3	450	10	095ZT1	095ZT1 arbidopsin
24	30	83.3	456	5	046078	046078 drosophila
25	30	83.3	463	16	09X143	09X143 thermotoga
26	30	83.3	499	2	0936Y8	0936Y8 pseudomonas
27	30	83.3	563	3	08X050	08X050 neuropept
28	30	83.3	743	11	08R5D1	08R5D1 mus musculu
29	30	83.3	1165	16	099XX8	099XX8 streptococc
30	30	83.3	2340	12	08U2Z7	08U2Z7 oat mosaic
31	29	80.6	140	2	099072	099072 desulfitoba
32	29	80.6	140	2	09AEH3	09AEH3 desulfitoba
33	29	80.6	156	2	09ACE4	09ACE4 uncultured
34	29	80.6	156	2	09ACF3	09ACF3 uncultured
35	29	80.6	156	2	09ACF2	09ACF2 uncultured
36	29	80.6	156	2	09ACF1	09ACF1 uncultured
37	29	80.6	189	2	09AEH0	09AEH0 dehalobacte
38	29	80.6	198	2	09AC94	09AC94 desulfitoba
39	29	80.6	198	2	09AC93	09AC93 desulfitoba
40	29	80.6	199	2	09AEH3	09AEH3 desulfitoba
41	29	80.6	243	17	082VW5	082VW5 pyrobaculum
42	29	80.6	252	5	09VK12	09VK12 drosophila
43	29	80.6	310	2	0939S6	0939S6 desulfitoba
44	29	80.6	316	2	0939S5	0939S5 desulfitoba
45	29	80.6	316	2	0939S3	0939S3 desulfitoba

ALIGNMENTS

RESULT 1

007550 PRELIMINARY; PRT; 585 AA.

AC 007550; 01-JUN-1997 (T-EMBLrel. 04, Created)

DT 01-JUN-1997 (T-EMBLrel. 04, last sequence update)

DT 01-JUN-2002 (T-EMBLrel. 21, last annotation update)

DE Hypothetical protein yhel.

GN YHE1.

OS Bacillus subtilis.

OC Bacteria; Firmicutes; Bacillus/Clostridium group; Bacillales;

CC Bacillaceae; Bacillus.

OX NCBI_TaxID:1423;

RA [1]

RP SEQUENCE FROM N.A.

RC STRAIN-168;

RL submitted (JUN-1997) to the EMBL/Genbank/DBJ databases.

RN [2]

RP SEQUENCE FROM N.A.

RC MEDLINE-98044033; PubMed-9384377;

RA Kunst F., Ogatawara N., Moser I., Albertini A.M., Alloni G.,

RA Azevedo V., Bertolo M.G., Hestieres P., Bolotin A., Borchert S.,

RA Borris R., Boursier L., Brans A., Braun M., Brignell S.C., Bron S.,

RA Brouillet S., Bruschi C.V., Caldwell B., Capuano V., Carter N.M.,

RA Choi S.K., Codani J.J., Connerion I.F., Cummings N.J., Daniel R.A.,

RA Denizot F., Devine K.M., Dusterhoft A., Ehrlich S.D., Emmerling P.T.,

08RUB2 oryza sativ
091TF3 oat mosaic
091TF2 oat mosaic
08VAX2 bruceella me
0917X6 drosophila
091BP9 oat mosaic
095ZT1 arbidopsin
046078 drosophila
09X143 thermotoga
0936Y8 pseudomonas
08X050 neuropept
099XX8 mus musculu
099XX8 streptococc
08U2Z7 oat mosaic
099072 desulfitoba
09AEH3 desulfitoba
09ACE4 uncultured
09ACF3 uncultured
09ACF2 uncultured
09ACF1 uncultured
09AEH0 dehalobacte
09AC94 desulfitoba
09AC93 desulfitoba
09AEH3 desulfitoba
082VW5 pyrobaculum
09VK12 drosophila
0939S6 desulfitoba
0939S5 desulfitoba
0939S3 desulfitoba

Enlign K.D., Enlignon J., Fabret C., Ferrari E., Foulger D.,
Fritz C., Fujita M., Fujita Y., Fuma S., Galizzi A., Galleron N.,
Ghim S.Y., Glaser P., Goffeau A., Gollightly E.J., Grandi G.,
Hilbert H., Holsappel S., Hosono S., Hullo M.F., Itaya M., Jones L.,
Kobayashi Y., Kariwata D., Kasahara Y., Klatir-Blanchard M., Klein C.,
Kobayashi Y., Koetter P., Koningsstein G., Krogh S., Kumano M.,
Kurita K., Lapiere A., Lardinois S., Lauer J., Lazarevic V.,
Lee S.M., Levine A., Liu H., Masuda S., Mauel C., Medigue C.,
Medina N., Mellado R.P., Mizuno M., Mostl D., Nakai S., Noback M.,
Moore D., O'Reilly M., Ogawa K., Ogiwara A., Oudega B., Patk S.H.,

RA Parro V., Pohl T.M., Portetelle D., Portollik S., Prescott A.M.,
RA Prescan E., Pujic P., Purnelle B., Rapoport G., Rey M., Reynolds S.,
RA Rieger M., Rivolta C., Rocha E., Roche B., Rose M., Sadale Y.,
RA Sato T., Scanlan E., Schleich S., Schroeter R., Scotone F.,
RA Sekiguchi J., Sekowska A., Seror S.J., Serro P., Shin B.S., Soldo B.,
RA Sorokin A., Taccioni E., Takagi T., Takahashi H., Takemaru K.,
RA Takeuchi M., Takakoshi A., Tanaka T., Terpiltra P., Tognoni A.,
RA Tosato V., Uchiyama S., Vandenbol M., Vannier F., Vassaretli A.,
RA Viari A., Wambutt R., Wedler E., Wedler H., Weitzenger T.,
RA Winters P., Wipat A., Yamamoto H., Yamane K., Yasumoto K., Yata K.,
RA Yoshida K., Yoshikawa H.F., Zumbstein E., Yoshikawa H., Danchin A.,
RT "The complete genome sequence of the gram-positive bacterium *Bacillus*
RT *subtilis*,"
RL Nature 390:249-256(1997).
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN-168;
RA Kunst F., Ogasawara N., Yoshikawa H., Danchin A.;
RL Submitted (NOV-1997) to the EMBL/Genbank/DBJ databases.
CC -1- SIMILARITY: BELONGS TO THE ATP-BINDING TRANSPORT PROTEIN FAMILY
CC (ABC TRANSPORTERS).
DR EMBL: Y14080; CAAT4450.1; -;
DR EMBL: Z99109; CAB12810.1; -;
DR HSSP: P13569; INED.
DR Interpro: IPR003593; AAA_ATPase.
DR Interpro: IPR001140; ABCtransportTM.
DR Interpro: IPR003439; ABC_transport.
DR Pfam: PF00664; ABC_membrane_1.
DR Pfam: PF00005; ABC_tran; 1.
DR ProDom: PD000006; ABC_transport; 1.
DR SMART: SM00382; AAA; 1.
DR PROSITE: PS00211; ABC_TRANSPORTER; 1.
DR ATP-binding; Hypothetical protein; Transport; Complete proteome.
SQ SEQUENCE 585 AA: 6511 MW; AB82FA64338F8161 CRC64;

Query Match 91.7%; Score 33; DB 16; Length 585;
Best Local Similarity 85.7%; Pred. No. 41;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 EKSRTGD 7
II:IIII
DB 110 EKNRTGD 116

RESULT 2
Q8X1A0 PRELIMINARY; PRT; 868 AA.
ID Q8X1A0;
AC Q8X1A0;
DT 01-MAR-2002 (Tremblrel. 20, Created)
DT 01-MAR-2002 (Tremblrel. 20, Last sequence update)
DT 01-JUN-2002 (Tremblrel. 21, Last annotation update)
DE Probable calcium-transporting ATPase.
GN CPEL202
OS Clostridium perfringens.
OC Bacteria; Firmicutes; Bacillus/Clostridium group; Clostridia;
OC Clostridiales; Clostridiaceae; Clostridium.
CC NCBI_TaxID=1502;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-13 / TYPE A;
RX PubMed=11792842;
RA Shima T., Ohtani K., Hirakawa H., Ohshima K., Yamashita A.,
RA Shiba T., Ogasawara N., Hattori M., Kihara S., Hayashi H.;
RT "Complete genome sequence of *Clostridium perfringens*, an anaerobic
RT flesh-eater,"
RL Proc. Natl. Acad. Sci. U.S.A. 99:996-1001(2002).
DR EMBL: AP003189; BAB80908.1; -;
DR Interpro: IPR001757; ATPase_E1-E2.
DR Interpro: IPR004014; Cation_ATPase.
DR Interpro: IPR000661; H/K_Na/K_ATPase.
DR Interpro: IPR001454; H1gnase/hydriase.
DR Interpro: IPR001245; Tyr_kinase.
DR Pfam: PF00689; Cation_ATPase_C; 1.

DR Pfam: PF00690; Cation_ATPase_N; 1.
DR PROSITE: PS00122; E1-E2_ATPase_1.
DR Pfam: PF00702; Hydrolase_1.
DR PRINTS: PRO0119; CARINPASE.
DR PROSITE: PS00154; ATPase_E1-E2; UNKNOWN.1.
DR PROSITE: PS00109; PROTEIN_KINASE_TYR; UNKNOWN.1.
DR Complete proteome.
SQ SEQUENCE 868 AA: 95746 MW; 1381A132261AC237 CRC64;

Query Match 88.9%; Score 32; DB 16; Length 868;
Best Local Similarity 85.7%; Pred. No. 11e+02;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 EKSRTGD 7
II:IIII
DB 376 EKSQTGD 382

RESULT 3
Q9VD20 PRELIMINARY; PRT; 1118 AA.
ID Q9VD20;
AC Q9VD20;
DT 01-MAY-2000 (Tremblrel. 13, Created)
DT 01-MAY-2000 (Tremblrel. 13, Last sequence update)
DT 01-JUN-2002 (Tremblrel. 21, Last annotation update)
DE CG18427 protein.
GN CG18427 OR CG12757.
OS Drosophila melanogaster (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Insecta;
OC Eukaryota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephyridioidea; Drosophilidae; Drosophila.
CC NCBI_TaxID=7227;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-BERKELEY;
RX MEDLINE=20196006; PubMed=10731132;
RA Adams M.D., Gelinkner S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Aamathides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA Sulten G.G., Mortan J.R., Yandell M.D., Zhang Q., Chen L.X.,
RA Brandon R.C., Rogers Y.-H.C., Blazek R.G., Champe M., Pfeiffer B.D.,
RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
RA April J.F., Abpayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,
RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
RA Beeson K.Y., Benos P.V., Bertan B.P., Bhandari D., Bolshakov S.,
RA Borokova D., Botchan M.R., Bouck J., Brockstein P., Brotler P.,
RA Burlis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
RA Cherry J.M., Cavley S., Dahlke C., Davenport L.B., Davies P.,
RA de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA Durbin K.J., Evangelista C.C., Ferraz C., Ferreira S., Fleischmann W.,
RA Foster C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K.,
RA Glodok A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
RA Harris N.L., Harvey D., Helman T.J., Hernandez J.R., Houck J.,
RA Hostli D., Houston K.A., Howland T.J., Wei M.-H., Idegyem C.,
RA Jaitai M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
RA Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
RA Liu X., Matei B., McIntosh T.C., McLeod M.P., McPherson D.,
RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshier A.,
RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Paclad J.M.,
RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
RA Shue B.C., Siden-Kiamos I., Simpson M., Skipski M.P., Smith T.,
RA Spier E.C., Spradling A.C., Stapleton M., Strong R., Sun E.,
RA Svraksas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
RA Wang Z.-Y., Wassarman D.A., Weinstein G.M., Weissbach J.,
RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
RA Ye J., Yen K.-E., Zaveri J.S., Zhan M., Zhan G., Zhao Q., Zheng L.,
RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
RT "The genome sequence of *Drosophila melanogaster*,"

RL Science 287:2185-2195(2000).
CC -1- CATALYTIC ACTIVITY: SN-GLYCEROL 3-PHOSPHATE + NAD(+) - GLYCERONE
CC PHOSPHATE + NADH.
CC -1- SIMILARITY: BELONGS TO THE NAD-DEPENDENT GLYCEROL-3-PHOSPHATE
CC DEHYDROGENASE FAMILY.
DR EMBL: AE003738; AAF5983.1; -.
DR FLYbase: FBgn0038955; CG18427.
DR InterPro: IPR001652; NAD_Gly3P_dh.
DR Pfam: PF01210; NAD_Gly3P_dh.1.
DR PRINTS: PR00077; GPDHGNASE.
KW NAD: Oxidoreductase.
SQ SEQUENCE 1118 AA; 125080 MW; 356E3746E9559ED6 CRC64;

Query Match 88.9%; Score 32; DB 5; Length 1118;
Best Local Similarity 85.7%; Pred. No. 1.5e+02;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 EKSRTGD 7
Db 986 EKDRGTG 992

RESULT 4
08T8S8 PRELIMINARY; PRT; 1186 AA.
AC 08T8S8.
DT 01-JUN-2002 (TREMBlrel. 21, Created)
DT 01-JUN-2002 (TREMBlrel. 21, last sequence update)
DT 01-JUN-2002 (TREMBlrel. 21, last annotation update)
DE AT30755p.
GN CG18427.
OS Drosophila melanogaster (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
OC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
OX NCBI_TaxID=7227;
RN [1]
RP SEQUENCE FROM N.A.
RA Stapleton M., Brokstein P., Hong L., Aghayani A., Carlson J.,
RA Champe M., Chavez C., Dorsett V., Dresnek D., Farfan D., Frise E.,
RA George R., Gonzalez M., Guarin H., Krommiller B., Li P., Liao G.,
RA Miranda A., Mungall C.J., Nunoo J., Pacled J., Paragas V., Park S.,
RA Patel S., Phouanavong S., Wan K., Yu C., Lewis S.E., Rubin G.M.,
RA Cealiker S.;
RL Submitted (JAN-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL: AY075291; AAL68158.1; -.
SQ SEQUENCE 1186 AA; 133529 MW; EC2606999C5EP36A CRC64;

Query Match 88.9%; Score 32; DB 5; Length 1186;
Best Local Similarity 85.7%; Pred. No. 1.6e+02;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 EKSRTGD 7
Db 1054 EKDRGTG 1060

RESULT 5
09BBS7 PRELIMINARY; PRT; 1332 AA.
AC 09BBS7.
DT 01-JUN-2001 (TREMBlrel. 17, Created)
DT 01-JUN-2001 (TREMBlrel. 17, last sequence update)
DT 01-JUN-2002 (TREMBlrel. 21, last annotation update)
DE RNA polymerase beta' subunit-2.
GN PPOC2.
OS Lotus japonicus.
OC Chloroplast.
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eurosids I; Fabales; Fabaceae; Papilionoideae; Lotaeae; Lotus.
OX NCBI_TaxID=34305;
RN [1]

RP SEQUENCE FROM N.A.
RC STRAIN-ACCESSION MG-20;
RA Kato T.;
RL Submitted (DEC-2000) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN-ACCESSION MG-20;
RC MEDLINE-21082929; PubMed-11214967;
RX Kato T., Kaneko T., Sato S., Nakamura Y., Tabata S.;
RT "Complete structure of the chloroplast genome of a legume, Lotus
RT japonicus.";
RT DNA Res. 7:323-330(2000).
RL EMBL: AP002983; BAB3196.1; -.
DR HSSP: O9KWU6; IHOM.
DR InterPro: IPR000722; RNA_POL_A.
DR InterPro: IPR002879; RNA_POL_A2.
DR Pfam: PF00623; RNA_POL_A; 1.
DR Pfam: PF01854; RNA_POL_A2; 2.
KW Chloroplast.
SQ SEQUENCE 1332 AA; 151852 MW; BDA32FF920B2B8C1 CRC64;

Query Match 88.9%; Score 32; DB 8; Length 1332;
Best Local Similarity 85.7%; Pred. No. 1.8e+02;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 EKSRTGD 7
Db 1112 EKSRSGD 1118

RESULT 6
09WTM3 PRELIMINARY; PRT; 1386 AA.
AC 09WTM3.
DT 01-OCT-2000 (TREMBlrel. 15, Created)
DT 01-OCT-2000 (TREMBlrel. 15, last sequence update)
DT 01-JUN-2002 (TREMBlrel. 21, last annotation update)
DE RNA polymerase beta' subunit.
GN PPOC2.
OS Oenothera hookeri (Hooker's evening primrose).
OC Chloroplast.
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eurosids II; Myrtales; Onagraceae; Oenothera.
OX NCBI_TaxID=85636;
RN [1]
RP SEQUENCE FROM N.A.
RA MEDLINE-20309318; PubMed-10852478;
RA Hupfer H., Swiatek M., Hohnung S., Herrmann R.G., Maier R.M.,
RA Chiu W.L., Sears B.;
RT "Complete nucleotide sequence of the Oenothera elata plastid
RT chromosome, representing plastome I of the five distinguishable
RT Eucnothera plastomes.";
RL Mol. Gen. Genet. 263:581-585(2000).
DR EMBL: AJ271079; CAB67153.1; -.
DR HSSP: O9KWU6; IHOM.
DR InterPro: IPR000722; RNA_POL_A.
DR InterPro: IPR002879; RNA_POL_A2.
DR Pfam: PF00623; RNA_POL_A; 1.
DR Pfam: PF01854; RNA_POL_A2; 2.
KW Chloroplast.
SQ SEQUENCE 1386 AA; 157202 MW; 720B5DAC30AD5ED0 CRC64;

Query Match 88.9%; Score 32; DB 8; Length 1386;
Best Local Similarity 85.7%; Pred. No. 1.9e+02;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 EKSRTGD 7
Db 1134 EKSRSGD 1140

RESULT 7

0858Y1
ID 0858Y1 PRELIMINARY; PRT; 1389 AA.
AC 0858Y1:
DT 01-JUN-2002 (TREMBlrel. 21, Created)
DT 01-JUN-2002 (TREMBlrel. 21, Last sequence update)
DT 01-JUN-2002 (TREMBlrel. 21, Last annotation update)
DE RNA polymerase Beta II subunit.
GN RPOC2.
OS *Atropa belladonna* (Belladonna) (Deadly nightshade).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
OC Asteridae; eumasterias I; Solanales; Solanaceae; *Atropa*.
OX NCBI_TaxID=33113;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=ABSP(KAN);
RA Schmitz-Lineweber C., Regel R., Gla Du T., Hupfer H., Hermann R.G.,
RA Maier R.M.;
RT "The nucleotide sequence of the plastid chromosome of *Atropa*
RT belladonna (deadly nightshade) and its comparison with that of
RT Nicotiana tabacum with emphasis on sequence elements relevant for
RT microevolution."
RL Submitted (MAY-2000) to the EMBL/GenBank/DDbJ databases.
DR EMBL; AJ316582; CAC88034.1; -
SQ SEQUENCE 1389 AA; 156857 MW; 987B9E096CB4BD5 CRC64;

Query Match 88.9%; Score 32; DB 10; Length 1389;
Best Local Similarity 85.7%; Pred. No. 1.9e+02;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 EKSRTGD 7
ID 11111111
Db 1136 EKSRSQD 1142

RESULT 8
ID 09AG08 PRELIMINARY; PRT; 132 AA.
AC 09AG08:
DT 01-JUN-2001 (TREMBlrel. 17, Created)
DT 01-JUN-2001 (TREMBlrel. 17, Last sequence update)
DT 01-JUN-2002 (TREMBlrel. 21, Last annotation update)
DE Ribosomal binding factor A.
GN RBFA.
OS *Molbachia* sp. wRI.
OC Bacteria; Proteobacteria; alpha subdivision; Rickettsiales;
OC Rickettsiaceae; *Molbachia*; *Molbachia*.
OX NCBI_TaxID=66084;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=WR1;
RA Sun L.Y., O'Neill S.L.;
RT "Genomic organization of the upstream region of the *Molbachia* dnaA
RT gene."
RL Submitted (FEB-2001) to the EMBL/GenBank/DDbJ databases.
DR EMBL; AF348350; AAK1136.1; -
DR InterPro; IPR000238; Rib_bind_facct.
DR Pfam; PF02033; RBFA.1;
SQ SEQUENCE 132 AA; 15102 MW; 24BCF395FA3CCADF CRC64;

Query Match 86.1%; Score 31; DB 2; Length 132;
Best Local Similarity 85.7%; Pred. No. 22;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 EKSRTGD 7
ID 11111111
Db 66 EKRRITGD 72

RESULT 9
ID 082969 PRELIMINARY; PRT; 248 AA.
AC 082969:

DT 01-NOV-1998 (TREMBlrel. 08, Created)
DT 01-NOV-1998 (TREMBlrel. 08, Last sequence update)
DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
DE A2-5a orf1 (Fragment).
OS *Bacillus* sp.
OC Bacteria; Firmicutes; *Bacillus*/Clostridium group; Bacillales;
OC Bacillaceae; *Bacillus*.
OX NCBI_TaxID=1409;
RN [1]
RP SEQUENCE FROM N.A.
RC MEDLINE=20261044; PubMed=10803899;
RA Ouden R., Kuriki T., Takata H., Okada S.;
RT "Cloning of the cyclodextrin glucanotransferase gene from alkalophilic
RT *Bacillus* sp. A2-5a and analysis of the raw starch-binding domain."
RL Appl. Microbiol. Biotechnol. 53:430-434 (2000).
DR EMBL; AB015670; BAA31529.1; -
FT NON_TER 1
SQ SEQUENCE 248 AA; 27286 MW; DB9322A115442722 CRC64;

Query Match 86.1%; Score 31; DB 2; Length 248;
Best Local Similarity 85.7%; Pred. No. 45;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 EKSRTGD 7
ID 11111111
Db 148 EKSRSQD 154

RESULT 10
ID 08RWD7 PRELIMINARY; PRT; 281 AA.
AC 08RWD7:
DT 01-JUN-2002 (TREMBlrel. 21, Created)
DT 01-JUN-2002 (TREMBlrel. 21, Last sequence update)
DT 01-JUN-2002 (TREMBlrel. 21, Last annotation update)
DE Hypothetical 31.6 kDa protein.
GN ARI638210.
OS *Arabidopsis thaliana* (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eurosids II; Brassicales; Brassicaceae; *Arabidopsis*.
OX NCBI_TaxID=3702;
RN [1]
RP SEQUENCE FROM N.A.
RA Southwick A., Katlin-Neumann G., Nguyen M., Lam B., Miranda M.,
RA Palm C.J., Bowser L., Jones T., Banh J., Carninci P., Chen H.,
RA Cheuk R., Chung M.K., Hayashizaki Y., Ishida J., Kamiya A., Kawai J.,
RA Kim C., Lin J., Liu S.X., Narusaka M., Pham P.K., Sakano H.,
RA Sakurai T., Satou M., Seki M., Shin P., Yamada K., Shinozaki K.,
RA Ecker J., Theologis A., Davis R.W.;
RL Submitted (MAR-2002) to the EMBL/GenBank/DDbJ databases.
DR EMBL; AY091160; AAM3159.1; -
KW Hypothetical protein.

Query Match 86.1%; Score 31; DB 10; Length 281;
Best Local Similarity 85.7%; Pred. No. 52;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 EKSRTGD 7
ID 11111111
Db 212 EKSRVGD 218

RESULT 11
ID 099V04 PRELIMINARY; PRT; 646 AA.
AC 099V04:
DT 01-JUN-2001 (TREMBlrel. 17, Created)
DT 01-JUN-2001 (TREMBlrel. 17, Last sequence update)
DT 01-MAR-2002 (TREMBlrel. 20, Last annotation update)
DE Hypothetical protein SAV0719.
GN SAV0719 OR SA0674.

OS Staphylococcus aureus (strain Mu50 / ATCC 700699), and
 OS Staphylococcus aureus (strain N315).
 OC Bacteria; Firmicutes; Bacillus/Clostridium group; Bacillales;
 OC Staphylococcus.
 ON NCBI_TaxID=158878, 158879;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC SPECIES=Staphylococcus aureus (strain Mu50), and S.aureus (strain N315);
 RX MEDLINE=21311952, PubMed=11418146;
 RA Kuroda M., Ohta T., Ochiyama T., Baba T., Yuzawa H., Kobayashi I.,
 RA Cut L., Oguchi A., Aoki K.-I., Nagai Y., Lan J.-O., Ito T.,
 RA Kanamori M., Matsumaru H., Maruyama A., Murakami H., Hosoyama A.,
 RA Mizutani U.I., Takahashi N.K., Sawano T., Inoue R.-I., Kaito C.,
 RA Sekimizu K., Hirakawa H., Kubara S., Goto S., Yabuzaki J.,
 RA Kanehisa M., Yamashita A., Oshima K., Furuya K., Yoshino C., Shiba T.,
 RA Hattori M., Ogasawara N., Hayashi K., Hiratsuka K.;
 RT *Whole genome sequencing of methicillin-resistant Staphylococcus
 RT aureus.
 RL Lancet 357:1225-1240(2001).
 DR EMBL: AP003360; BAB56881.1; -
 DR EMBL: AP003361; BAB41907.1; -
 DR InterPro: IPR000917; Sulfatase.
 DR Pfam: PF00884; Sulfatase; 1.
 KW Hypothetical protein: Complete proteome.
 SQ SEQUENCE 646 AA; 74400 MW; 788FE36EB4528BB0 CRC64;
 OY Query Match 86.1%; Score 31; DB 16; Length 646;
 Best Local Similarity 85.7%; Pred. No. 1.4e+02;
 Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 Db 429 EKSRTGD 435
 OY 1 EKSRTGD 7
 Db 111 111
 Db 429 EKSRTGD 435
 RESULT 12
 OY 09C730 PRELIMINARY; PRT: 1195 AA.
 ID 09C730
 AC 09C730
 DT 01-JUN-2001 (TReMBLrel. 17, Created)
 DT 01-JUN-2001 (TReMBLrel. 17, last sequence update)
 DT 01-JUN-2001 (TReMBLrel. 17, last annotation update)
 DE Hypothetical 135.5 kDa protein.
 GN F16W22.3.
 OS Arabidopsis thaliana (Mouse-ear cress).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
 OC eustosids II; Brassicales; Brassicaceae; Arabidopsis.
 ON NCBI_TaxID=3702;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=CV, COLUMBIA;
 RX MEDLINE=21016719; PubMed=11130712;
 RA Theologis A., Ecker J.R., Palm C.J., Federspiel N.A., Kaul S.,
 RA White O., Alonso J., Altafi H., Araujo R., Bowman C.L., Brooks S.Y.,
 RA Buehler E., Chan A., Chao O., Chen H., Cheuk R.F., Chin C.W.,
 RA Chung M.K., Conn L., Conway A.B., Creasy T.H., Dewar K.,
 RA Dunn P., Elgu P., Feldblyum T.V., Feng J.-D., Fong B., Fujii C.Y.,
 RA Gill J.E., Goldsmith A.D., Haas B., Hansen N.F., Hughes B., Huizar L.,
 RA Hunter J.L., Jenkins J., Johnson-Hopson C., Khan S., Khaykin E.,
 RA Kim C.J., Koo H.L., Kremetska I., Kurtz D.B., Kwan A., Lam B.,
 RA Langin-Hooper S., Lee A., Lee J.M., Lenz C.A., Li J.H., Li Y.-P.,
 RA Lin X., Liu S.X., Liu Z.A., Luros J.S., Maiti R., Marziani A.,
 RA Millischer J., Miranda M., Nguyen M., Nierman W.C., Osborne B.I.,
 RA Sakano H., Salzer S.L., Schwartz J.R., Shim P., Southwick A.M.,
 RA Sun H., Tallon L.J., Tambunga G., Toriumi M.J., Town C.D.,
 RA Uterback T., Van Aken S., Vaysberg M., Vysotska V.S., Walker M.,
 RA Wu D., Yu G., Fraser C.M., Venter J.C., Davis R.W.;
 RT *Sequence and analysis of chromosome 1 of the plant Arabidopsis
 RT thaliana.*
 RL Nature 408:816-820(2000).
 DR EMBL: AC073943; AAG50957.1; -
 DR EMBL: AC073943; AAG50957.1; -

DR InterPro: IPR001064; Crystallin.
 DR PROSITE: PS00225; CRYSTALLIN_BETAGAMMA; UNKNOWN_1.
 KW Hypothetical protein.
 SQ SEQUENCE 1195 AA; 135520 MW; 6EFE58DCE994D744 CRC64;
 OY Query Match 86.1%; Score 31; DB 10; Length 1195;
 Best Local Similarity 85.7%; Pred. No. 2.7e+02;
 Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 Db 212 EKSRTGD 218
 OY 1 EKSRTGD 7
 Db 111 111
 Db 212 EKSRTGD 218
 RESULT 13
 OY 09C609 PRELIMINARY; PRT: 1246 AA.
 ID 09C609
 AC 09C609
 DT 01-JUN-2001 (TReMBLrel. 17, Created)
 DT 01-JUN-2001 (TReMBLrel. 17, last sequence update)
 DT 01-JUN-2001 (TReMBLrel. 17, last annotation update)
 DE Hypothetical 141.0 kDa protein.
 GN T18124.12.
 OS Arabidopsis thaliana (Mouse-ear cress).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
 OC eustosids II; Brassicales; Brassicaceae; Arabidopsis.
 ON NCBI_TaxID=3702;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=CV, COLUMBIA;
 RX MEDLINE=21016719; PubMed=11130712;
 RA Theologis A., Ecker J.R., Palm C.J., Federspiel N.A., Kaul S.,
 RA White O., Alonso J., Altafi H., Araujo R., Bowman C.L., Brooks S.Y.,
 RA Buehler E., Chan A., Chao O., Chen H., Cheuk R.F., Chin C.W.,
 RA Chung M.K., Conn L., Conway A.B., Creasy T.H., Dewar K.,
 RA Dunn P., Elgu P., Feldblyum T.V., Feng J.-D., Fong B., Fujii C.Y.,
 RA Gill J.E., Goldsmith A.D., Haas B., Hansen N.F., Hughes B., Huizar L.,
 RA Hunter J.L., Jenkins J., Johnson-Hopson C., Khan S., Khaykin E.,
 RA Kim C.J., Koo H.L., Kremetska I., Kurtz D.B., Kwan A., Lam B.,
 RA Langin-Hooper S., Lee A., Lee J.M., Lenz C.A., Li J.H., Li Y.-P.,
 RA Lin X., Liu S.X., Liu Z.A., Luros J.S., Maiti R., Marziani A.,
 RA Millischer J., Miranda M., Nguyen M., Nierman W.C., Osborne B.I.,
 RA Sakano H., Salzer S.L., Schwartz J.R., Shim P., Southwick A.M.,
 RA Sun H., Tallon L.J., Tambunga G., Toriumi M.J., Town C.D.,
 RA Uterback T., Van Aken S., Vaysberg M., Vysotska V.S., Walker M.,
 RA Wu D., Yu G., Fraser C.M., Venter J.C., Davis R.W.;
 RT *Sequence and analysis of chromosome 1 of the plant Arabidopsis
 RT thaliana.*
 RL Nature 408:816-820(2000).
 DR EMBL: AC079131; AAG50760.1; -
 DR InterPro: IPR001064; Crystallin.
 DR PROSITE: PS00225; CRYSTALLIN_BETAGAMMA; UNKNOWN_1.
 KW Hypothetical protein.
 SQ SEQUENCE 1246 AA; 140995 MW; BE23E9DC4F3F88 CRC64;
 OY Query Match 86.1%; Score 31; DB 10; Length 1246;
 Best Local Similarity 85.7%; Pred. No. 2.9e+02;
 Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 Db 212 EKSRTGD 218
 OY 1 EKSRTGD 7
 Db 111 111
 Db 212 EKSRTGD 218
 RESULT 14
 OY 082TW7 PRELIMINARY; PRT: 79 AA.
 ID 082TW7
 AC 082TW7
 DT 01-MAR-2002 (TReMBLrel. 20, Created)
 DT 01-MAR-2002 (TReMBLrel. 20, last sequence update)
 DT 01-JUN-2002 (TReMBLrel. 21, last annotation update)

Search completed: November 12, 2002, 17:00:20
 Job time : 4.13305 secs

DE Hypothetical protein PAE3058.
 CN PAE3058.
 OS Pyrobaculum aerophilum.
 OC Archaea: Crenarchaeota: Thermoprotei: Thermoproteales;
 OC Thermoproteaceae: Pyrobaculum.
 OX NCBI_TaxID=13773;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=IM2 / ATCC 51768 / DSM 7523;
 RX PubMed=11792869;
 RA Flitz-Gibbon S.T., Ladner H., Kim U.-J., Stetter K.O., Simon M.I.,
 Miller J.H.;
 RT "Genome sequence of the hyperthermophilic crenarchaeon Pyrobaculum
 aerophilum.";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:984-989(2002).
 DR EMBL: AE009908; AAL6462.1; -.
 DR InterPro: IPR002792; TRAM.
 DR Pfam: PF01938; TRAM: 1
 KH Hypothetical protein; Complete proteome.
 SQ SEQUENCE 79 AA: 8695 MW: 83605871B6C30143 CRC64:

Query Match 83.3%; Score 30; DB 17; Length 79;
 Best Local Similarity 85.7%; Pred. No. 21;
 Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 EKSRTGD 7
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 DB 34 EKSRTGD 40

RESULT 15

Q8UK19
 ID Q8UK19 PRELIMINARY; PRT; 92 AA.
 AC Q8UK19;
 DT 01-JUN-2002 (TrEMBLrel. 21, Created)
 DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
 DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
 DE Transcriptional regulator.
 GN ATU5113.
 OS Agrobacterium tumefaciens (strain C58 / ATCC 33970).
 OC Plasmid AT.
 OC Bacteria: Proteobacteria; alpha subdivision: Rhizobiaceae group;
 OC Rhizobiaceae: Rhizobium.
 OX NCBI_TaxID=176299;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=21608550; PubMed=11743193;
 RA Wood D.W., Setubal J.C., Kaul R., Monks D.E., Kitajima J.P.,
 Okura Y.K., Zhou Y., Chen L., Wood G.E., Almeida N.F. Jr., Woo L.,
 Chen Y., Paulsen I.T., Eisen J.A., Karp P.D., Boye D. Sr.,
 Chapman P., Clendening J., Deatherage G., Gillet M., Grant C.,
 Kutayyan T., Levy R., Li M.-J., McLelland E., Palmieri A.,
 Raymond C., Rouse G., Saenphimachak C., Wu Z., Romero P., Gordon D.,
 Zhang S., Yoo H., Tao Y., Biddle P., Jung M., Krespan W., Perry M.,
 Gordon-Kamm B., Liao L., Kim S., Hendrick C., Zhao Z.-Y., Dolan M.,
 Chumley F., Tingey S.V., Tomb J.-F., Gordon M.P., Olson M.V.,
 Nester E.W.;
 RT "The genome of the natural genetic engineer Agrobacterium tumefaciens
 C58.";
 RL Science 294:2317-2323(2001).
 DR EMBL: AE008936; AAL45803.1; -.
 KW Plasmid; Complete proteome.
 SQ SEQUENCE 92 AA: 10349 MW: 518379FD71DF6D2 CRC64:

Query Match 83.3%; Score 30; DB 16; Length 92;
 Best Local Similarity 71.4%; Pred. No. 25;
 Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

OY 1 EKSRTGD 7
 |||||
 DB 21 ERARTGD 27

GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on: November 12, 2002, 16:48:46 ; Search time 16.0429 Seconds
(without alignments)
348.847 Million cell updates/sec

Title: US-09-848-271-2_COPY_4_45

Perfect score: 239
Sequence: 1 MAGOCSQNEHYFDLHACIP.....LRCSNTPPLTCGRYCNASV 42

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 908470 seqs, 133250620 residues

Total number of hits satisfying chosen parameters: 908470

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

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2: /SID2/gcgdata/geneseq/geneseq-emb1/AA1981.DAT:*
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4: /SID2/gcgdata/geneseq/geneseq-emb1/AA1983.DAT:*
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22: /SID2/gcgdata/geneseq/geneseq-emb1/AA2001.DAT:*
23: /SID2/gcgdata/geneseq/geneseq-emb1/AA2002.DAT:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	239	100.0	51	23	AAE15485 Human B-cell matur
2	239	100.0	181	23	AAE15484 Human B-cell matur
3	239	100.0	184	21	AAE08843 Amino acid sequenc
4	239	100.0	184	21	AA194001 Human BCMA protei
5	239	100.0	184	22	AAE05241 Human BCMA protei
6	239	100.0	184	22	AAE05056 Human B cell matur
7	239	100.0	184	22	AAE05056 Human B cell matur
8	239	100.0	184	22	AAE05056 Human B cell matur
9	239	100.0	184	23	AAE05056 Human B cell matur
10	239	100.0	283	23	AAE15488 Human BCMA-Immunog

11	239	100.0	302	22	AAE00507 Human BCMA-Immunog
12	239	100.0	302	22	AAE06999 Mouse IgG signal/h
13	219	91.6	58	22	AAE15501 Human B cell matur
14	201	84.1	34	23	AAE15486 Human B-cell matur
15	181	75.7	157	22	AAE06700 Human BAFR recepto
16	156	65.3	185	21	AAE08844 Amino acid sequenc
17	156	65.3	185	21	AAE08844 Amino acid sequenc
18	156	65.3	185	22	AAE15490 Mouse B cell matur
19	156	65.3	185	22	AAE15489 Mouse B cell matur
20	95.5	40.0	117	23	AAE15489 Mouse BCMA-human 1
21	90.5	37.9	24	23	AAE15492 Human-murine BCMA
22	71.5	29.9	249	21	AAE15492 A murine ztnf4, a
23	67.5	28.2	37	23	AAE15500 Human AGP-3 recept
24	67.5	28.2	59	23	AAE15500 Human TACI cystein
25	67.5	28.2	166	19	AAE15494 Human lymphocyte s
26	67.5	28.2	166	22	AAE15494 Human TACI extrace
27	67.5	28.2	265	22	AAE09244 Human TACI splice
28	67.5	28.2	291	23	AAU10949 Human Agp-3 recept
29	67.5	28.2	293	19	AAE15783 Human lymphocyte s
30	67.5	28.2	293	21	AAE15783 Human neutrokin-a
31	67.5	28.2	293	21	AAE15783 A transmembrane ac
32	67.5	28.2	293	22	AAE09240 Human tumor necro
33	67.5	28.2	293	22	AAE09240 Human TACI-196 Fc
34	67.5	28.2	293	23	AAE09240 Human TACI-196 Fc
35	67.5	28.2	293	23	AAE09240 Human TACI-196 Fc
36	67.5	28.2	293	23	AAE09240 Human TACI-196 Fc
37	67.5	28.2	293	23	AAE09240 Human TACI-196 Fc
38	67.5	28.2	293	23	AAE09240 Human TACI-196 Fc
39	67.5	28.2	293	23	AAE09240 Human TACI-196 Fc
40	67.5	28.2	293	23	AAE09240 Human TACI-196 Fc
41	67.5	28.2	312	23	AAE09240 Human TACI-196 Fc
42	67.5	28.2	312	23	AAE09240 Human TACI-196 Fc
43	67.5	28.2	366	23	AAE09240 Human TACI-196 Fc
44	67.5	28.2	397	23	AAE09240 Human TACI-196 Fc
45	66.5	28.2	404	23	AAE09240 Human TACI-196 Fc

ALIGNMENTS

RESULT 1	AAE15485	standard; peptide; 51 AA.
ID	AAE15485	standard; peptide; 51 AA.
AC	AAE15485	
XX		
DT	12-MAR-2002	(first entry)
XX		
DE	Human B-cell maturation (BCMA) protein extracellular domain.	
XX		
XX	Human: transmembrane activator and intracellular CAML interactor; TACI; cytosolic; B cell maturation protein; BCMA; tumor necrosis factor; TNF; lymphoproliferative disorder; tumor; lung; gastrointestinal; pancreatic; prostate; inflammation; immune disorder; diarrhoea; psoriasis; colitis; drug allergy; dermatitis; pneumonia; asthma; inflammatory bowel disease; Crohn's disease; scleroderma; autoimmune disease; multiple sclerosis; human immunodeficiency virus; HIV; systemic lupus erythematosus; cancer; rheumatoid arthritis; atherosclerosis.	
XX		
OS	Homo sapiens.	
XX		
PN	MO200187979-A2.	
XX		
PD	22-NOV-2001.	
XX		
PP	14-MAY-2001; 2001MO-US15567.	
XX		
PR	12-MAY-2000; 2000US-204039P.	
PR	27-JUN-2000; 2000US-214591P.	
PR	14-MAY-2001; 2001US-0214591.	
XX		
PA	(AMGE-) AMGEN INC.	
XX		

PD	XX	31-AUG-2000.
PX	XX	24-FEB-2000: 2000MO-US04925.
PF	XX	24-FEB-1999. 99US-0121485.
PR	XX	(GEHO) GEN HOSPITAL CORP.
PA	XX	Seed B, Ting A;
PI	XX	WPI: 2000-558405/51.
DR	XX	
XX	XX	
PT	XX	Identifying a modulator of gene expression for drug designing, by
PT	XX	contacting a compound library with a cell expressing an anti-cell death
PT	XX	gene and reporter gene, and determining alteration in reporter gene
PS	XX	expression -
PS	XX	Claim 32: Fig 7A; 53pp; English.
CC	XX	The present sequence represents a BCMA (not defined) polypeptide. BCMA
CC	XX	is a necrosis factor (NF)-KB activator. The method of the invention is
CC	XX	used to identify compounds which modulate BCMA activity (and thus NF-KB
CC	XX	activity). The specification describes a method of identifying a
CC	XX	polypeptide which increases gene expression from a promoter. The method
CC	XX	involves contacting a library of with a cell which expresses a
CC	XX	recombinant anti-cell death gene and a reporter gene operably linked to
CC	XX	the promoter, and then determining whether the expression of the
CC	XX	reporter gene is altered as a result of contact with library. The method
CC	XX	is useful for identifying polypeptides which increase or decrease gene
CC	XX	expression from a promoter. The BCMA polypeptide or nucleic acid are
CC	XX	useful for preparing a pharmaceutical composition for treating cancer,
CC	XX	apoptosis, viral infections, inflammatory response, such as rheumatoid
CC	XX	arthritis, inflammatory bowel disease or septic shock. BCMA is useful for
CC	XX	identifying compounds that modulate NF-KB expression and thus for drug
CC	XX	designing.
SQ	XX	Sequence 184 AA:
Query Match		100.0%; Score 239; DB 21; Length 184;
Best Local Similarity		100.0%; Pred. No. 1.7e-21;
Matches 42; Conservative		0; Mismatches 0; Indels 0; Gaps 0;
DQ	I	MAGGCGSNGEYFDSLHACTPCQLRCSSTNPPLTCGRYNASV 42
DB	4	MAGGCGSNGEYFDSLHACTPCQLRCSSTNPPLTCGRYNASV 45
RESULT 4		
AAY94001	ID	AAY94001 standard; Protein; 184 AA.
AC	XX	AAY94001;
DT	XX	20-OCT-2000 (first entry)
DE	XX	A human BCMA protein, a B cell protein related to TACI.
XX	XX	
KM	Human; BH4332; TACI receptor; extracellular domain; BCMA; B cell protein;	
KM	transmembrane activator and CAML-interactor; tumor necrosis factor; TNF;	
KM	Zn ²⁺ activity; antibody production; autoimmune disease; amyloidosis;	
KM	rheumatic lupus erythematosus; myasthenia gravis; multiple sclerosis;	
KM	rheumatoid arthritis; asthma; bronchitis; emphysema; pyelonephritis;	
KM	end stage renal failure; glomerulonephritis; vasculitis; nephritis;	
KM	renal neoplasms; multiple myeloma; lymphoma; light chain neuropathy;	
KM	immune response; immunosuppression; graft rejection; joint pain;	
KM	graft versus host disease; inflammation; swelling; anemia; septic shock;	
KM	insulin dependent diabetes mellitus; Crohn's disease; hypertension;	
KM	renal artery stenosis; occlusion; cholesterol; renal emboli.	
XX	XX	
DS	XX	Homo sapiens.
NN	XX	WO2000040716-A2.

PD	13-JUL-2000.	
XX		
XX	07-JAN-2000: 2000MO-US00396.	
XX		
PR	07-JAN-1999: 99US-0226533.	
XX		
PA	(ZYMO) ZYMOGENETICS INC.	
XX		
PI	Gross JA, Xu W, Madden K, Yee DP;	
DR	WPI: 2000-452538/39.	
XX	N-PSDB: AAA58559.	
PT	Inhibiting ztnf4 activity in a mammal, to treat autoimmune diseases,	
XX	renal disease, graft versus host disease, and inflammation, comprises	
XX	administering a BR43x2, TACI or BCMA extracellular domain polypeptide -	
PS	Disclosure; Page 152; 175pp; English.	
XX		
XX	The present sequence represents a human BCMA protein, a B cell protein	
CC	related to transmembrane activator and CAM1-interactor (TACI) receptor.	
CC	TACI is a tumour necrosis factor (TNF) receptor. The extracellular	
CC	domains of BR43x2 (an isoform of TACI), TACI or BCMA (a related B cell	
CC	protein) receptor contain a cysteine rich domain, and are used for	
CC	inhibiting ztnf4 activity. Ztnf4 is a TNF ligand. They may also be used	
CC	for inhibiting BR43x2, TACI or BCMA receptor-ligand engagement associated	
CC	with activated or resting B lymphocytes, effector T-cells, or with	
CC	antibody production. The antibody production is associated with an	
CC	autoimmune disease selected from systemic lupus erythematosus, myasthenia	
CC	gravis, multiple sclerosis and rheumatoid arthritis. The ztnf4 activity	
CC	and BR43x2, TACI or BCMA receptor-ligand engagement is associated with	
CC	asthma, bronchitis, emphysema, end stage renal failure,	
CC	glomerulonephritis, vasculitis, nephritis, pyelonephritis, renal	
CC	neoplasms, multiple myelomas, lymphomas, light chain neuropathy	
CC	amyloidosis, moderating immune response, immunosuppression, graft	
CC	rejection, graft versus host disease, inflammation, insulin dependent	
CC	diabetes mellitus, Crohn's disease, joint pain, swelling, anaemia, or	
CC	septic shock. BR43x2, TACI, and BCMA polypeptides, fusions, antibodies,	
CC	agonists or antagonists can be used to treat hypertension, renal artery	
CC	stenosis, or occlusion, and cholesterol or renal emboli.	
XX		
SO	Sequence 184 AA:	
YY		
Query Match	100.0%; Score 239; DB 21; Length 184;	
Best Local Similarity	100.0%; Pred. No. 1,7e-21;	
Matches 42; Conservative	0; Mismatches 0; Indels 0; Gaps 0;	
0y	1 MAGCCSONEYFDSLHACIPCOLRSSNPPTTCGRYCNASV 42	
Db	4 MAGCCSONEYFDSLHACIPCOLRSSNPPTTCGRYCNASV 45	
RESULT 5		
ID	AAE09241 standard; Protein; 184 AA.	
XX	AAE09241:	
AC		
XX		
DT	19-NOV-2001 (first entry)	
XX		
DE	Human BCMA protein.	
XX		
KW	Human; TNF; tumour necrosis factor; TAIL-1; APRIL; TNF receptor;	
KW	TNFR; TACI; BCMA; therapy; cancer; leukaemia; myeloma; lymphoma;	
KW	autoimmune disease; rheumatoid arthritis; multiple sclerosis;	
KW	psoriasis.	
XX		
OS	Homo sapiens.	
XX		
PN	WO200160397-A1.	
XX		
PD	23-AUG-2001	

```
XX 28-NOV-2000; 2000MO-US92378.
PF 16-FEB-2000; 2000US-0182938.
XX 22-AUG-2000; 2000US-0226986.
PR (GETH ) GENENTECH INC.
XX
XX Ashkenazi AJ, Dodge KH, Grewal I, Kim KJ, Marsters SA, Pletli RM;
PI Yan M;
XX WPI: 2001-541628/60.
DR N-PSDB; AAD15902.
XX
XX Inhibiting or neutralizing TALL-1 or APRIL polypeptide biological
PT activity, for treating autoimmune disorders and cancer, comprises
PT exposing the cells to TALL-1 or APRIL polypeptide agonists or
PT antagonists -
XX
XX Example 2; Fig 2; 160pp; English.
XX
XX The invention relates to methods of using one or more agonists or
CC antagonists to modulate the activity of the members of TNF (tumour
CC necrosis factor) especially TALL-1, APRIL and TNF receptor (TNFR)
CC e.g. TACI or BCMA. The method is useful for treating pathological
CC conditions or diseases associated with increased TALL-1 and APRIL
CC expression or activity. TALL-1 and APRIL antagonists are used to
CC block the interaction between APRIL and TALL-1 with TACI or BCMA.
CC They are useful for treating a mammal suffering from cancer such
CC as leukaemia, lymphoma, myeloma, cancers of lung and colon and
CC autoimmune diseases e.g. Rheumatoid arthritis, multiple sclerosis,
CC psoriasis and lupus erythematosus. The present sequence is human
CC BCMA protein.
XX
XX Sequence 184 AA;
SQ
Query Match 100.0%; Score 239; DB 22; Length 184;
Best Local Similarity 100.0%; Pred. No. 1.7e-21;
Matches 42; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 1 MAGGCSQNEVFDLSLHACIPQQLRCSSTPPLTCQRYCNASV 42
DB 4 MAGGCSQNEVFDLSLHACIPQQLRCSSTPPLTCQRYCNASV 45
RESULT 6
AAE00506
ID AAE00506 standard; Protein: 184 AA.
XX
XX AAE00506;
AC
XX
XX 31-JUL-2001 (first entry)
DT
XX
XX Human B cell maturation protein (BCMA).
DE
XX
XX Human; A Proliferation Inducing Ligand Receptor; APRIL-R; cytostatic;
KW gene therapy; cancer; nephrotic; renal disorder; autoimmune disease;
KW carcinoma; lung; colon; breast; prostate; Grave's disease; hypertension;
KW systemic lupus erythematosus; SLE; inflammation; cardiovascular disease;
KW B-cell lympho-proliferative disorder; BCM; immunosuppressive disease;
KW organ transplantation; HIV; human immunodeficiency virus; TNF;
KW tumour necrosis factor; BCMA; B cell maturation protein.
XX
XX Homo sapiens.
OS
XX
XX WO200124811-A1.
PN
XX
XX 12-APR-2001.
PD
XX
XX 05-OCT-2000; 2000MO-US27579.
PF
XX
XX 06-OCT-1999; 99US-0157933.
PR
XX
XX 11-FEB-2000; 2000US-0181807.
PR
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PR 30-JUN-2000; 2000US-0215688.
XX
XX (BIOJ ) BIOGEN INC.
PA (APOT-) APOTEC R & D SA.
XX
XX Schneider P, Thompson J, Cachero T, Ambrose C, Rennett P;
PI WPI: 2001-266242/27.
DR N-PSDB; AAD03844.
XX
XX Treating a mammal for a condition associated with undesired cell
PT proliferation such as cancer or carcinoma, comprises administering a
PT composition comprising A proliferation inducing Ligand Receptor
PT (APRIL-R) antagonist -
XX
XX Claim 3; Fig 3A; 85pp; English.
XX
XX The invention relates to a method of treating a mammal for a condition
CC associated with undesired cell proliferation such as cancer or
CC carcinoma. The method involves administering a composition comprising
CC A Proliferation Inducing Ligand Receptor (APRIL-R) also referred as
CC B cell maturation protein (BCM or BCMA) antagonist that antagonises the
CC interaction between APRIL and its cognate receptor(s). This method is
CC useful for treating undesired cell proliferation such as cancer or
CC carcinoma e.g. human lung carcinoma, colon carcinoma, breast carcinoma,
CC prostate carcinoma, and other carcinomas whose proliferation is modulated
CC by APRIL. It is also useful for treating autoimmune diseases (Grave's
CC disease, systemic lupus erythematosus-SLE), hypertension, cardiovascular
CC diseases, renal disorders, B-cell lympho-proliferative disorders,
CC immunosuppressive diseases, organ transplantation, inflammation and
CC altering an immune response involving a signalling pathway between
CC APRIL-R and its ligand. APRIL-R DNA is also useful in gene therapy.
CC The present sequence is human APRIL-R also referred as BCMA or
CC BCM protein.
XX
XX Sequence 184 AA;
SQ
Query Match 100.0%; Score 239; DB 22; Length 184;
Best Local Similarity 100.0%; Pred. No. 1.7e-21;
Matches 42; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 1 MAGGCSQNEVFDLSLHACIPQQLRCSSTPPLTCQRYCNASV 42
DB 4 MAGGCSQNEVFDLSLHACIPQQLRCSSTPPLTCQRYCNASV 45
RESULT 7
AAB60698
ID AAB60698 standard; Protein: 184 AA.
XX
XX AAB60698;
AC
XX
XX 22-MAY-2001 (first entry)
DT
XX
XX Human BAFF receptor (BAFF-R).
DE
XX
XX Human BAFF-R; BAFF receptor; TNF family; immunoregulatory agent;
KW immune-related disorder; B-cell growth inhibitor; BCM;
KW B-cell maturation inhibitor; immunoglobulin production inhibitor;
KW autoimmune disorder; B-cell lymphoproliferative disorder; hypertension;
KW renal disorder; immunosuppressive disorder; HIV infection;
KW organ transplantation; antinflammatory; systemic lupus erythematosus;
KW autoimmune haemolytic anaemia; Grave's disease; multiple myeloma;
KW B-cell carcinoma; leukaemia; rapidly progressive glomerulonephritis;
KW lymphoma; gene therapy; cancer; tumour.
XX
XX Homo sapiens.
OS
XX
XX WO200112812-A2.
PN
XX
XX 22-FEB-2001.
PD
XX
XX
```

PX	16-AUG-2000; 2000MO-US22507.
PR	17-AUG-1999; 98US-0149378.
PR	11-FEB-2000; 2000US-0181684.
PR	18-FEB-2000; 2000US-0183536.
XX	
PA	(BIOJ) BIOGEN INC.
PA	(APOT-) APOTECH R & D SA.
PI	Mackay F., Browning J., Ambrose C., Tschopp J., Schneider P;
PI	Thompson J;
DR	WPI: 2001-202866/20.
DR	N-PDB: AAF59998.
XX	
PT	Inhibiting dendritic cell-induced B-cell growth, maturation and B-cell
PT	lympho-proliferative disorder by administering BAFF-receptor
PT	polypeptide, chimeric molecule comprising receptor or anti-BAFF-R
PT	antibody homolog -
PS	Claim 20; Fig 1; 59pp; English.
XX	
CC	The invention relates to the use of a BAFF receptor (BAFF-R, also known
CC	as BCMA) protein, or a BAFF-R fusion protein as an agent for the
CC	treatment of a variety of immune-related disorders. BAFF-R is a member of
CC	the TNF (tumour necrosis factor) family, acting as an immunoregulatory
CC	agent, and also plays a role in the development of hypertension and
CC	related disorders. BAFF-R, fusion proteins containing it, and BAFF-R-
CC	specific antibodies can be used for inhibiting B-cell growth, dendritic
CC	cell-induced B-cell growth and maturation, and immunoglobulin production,
CC	and in the treatment of autoimmune disorders, B-cell lymphoproliferative
CC	disorders, hypertension and renal disorders. The BAFF-R proteins may also
CC	be used in the treatment of immunosuppressive disorders and HIV
CC	infection, and in patients undergoing organ transplantation. The BAFF-R
CC	proteins or BAFF-R specific antibodies may be used for treating,
CC	suppressing or altering an immune response involving a signalling pathway
CC	between BAFF-R and BAFF, thereby inhibiting inflammation. Since BAFF-R
CC	inhibits B-cell growth and maturation it is useful for treating diseases
CC	such as systemic lupus erythematosus, autoimmune haemolytic anaemia,
CC	Grave's disease, multiple myeloma, B-cell carcinomas, leukaemia, rapidly
CC	progressive glomerulonephritis, and lymphomas. Nucleic acids encoding
CC	human BAFF-R may be used in gene therapy to treat tumours, lymphomas,
CC	autoimmune disorders and inherited B-cell-associated disorders. The
CC	present sequence represents human BAFF-R.
CX	
SQ	Sequence 184 AA:
	Query Match 100.0%; Score 239; DB 22; Length 184;
	Best Local Similarity 100.0%; Pred. No. 1,7e-21;
	Matches 42; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY	
	1 MAGGSGNEVFDSLACTPCLRCSSNMPPLTCORGNASV 42
	4 MAGGSGNEVFDSLACTPCLRCSSNMPPLTCORGNASV 45
Db	
RESULT 8	
ID	AAAY71979
AC	AAV71979 standard; Protein; 184 AA.
XX	
XX	AAV71979:
DT	
DE	28-MAR-2001 (first entry)
XX	
XX	Human B cell maturation factor (BCMA) protein.
KW	Human Tumour Necrosis Factor; TNF; immunosuppressant; TALL-1;
KW	Tumour necrosis factor and Apol.-related leucocyte expressed ligand 1;
KW	therapy; autoimmune disorder; rheumatoid arthritis; multiple sclerosis;
KW	systemic lupus erythematosus; SLE; insulin dependent diabetes mellitus;
KW	thrombocytopenia purpura; acute rheumatic fever; Goodpasture's syndrome;
KW	haemolytic anaemia; Grave's disease; myasthenia gravis; chromosome 16;
KW	post-streptococcal glomerulonephritis; polyarteritis nodosa; BCMA;

XX	B	cell maturation factor; pemphigus vulgaris; B-lymphocyte proliferation.		
XX				
OS	Homo sapiens.			
FH	Key	Location/Qualifiers		
FT	Domain	1..62		
FT		/label= Extracellular_domain		
XX				
FN	MO2000068378-A1.			
XX				
FD	16-NOV-2000.			
XX				
FE	05-MAY-2000; 2000MO-US12266.			
XX				
PR	06-MAY-1999; 99US-0132892.			
PR	01-MAY-2000; 2000US-0201012.			
XX				
PA	(NAJE-) NAT JEWISH MEDICAL & RES CENT.			
XX				
FI	Shu HS:			
XX				
DR	WPI: 2001-016094/02.			
DR	N-PSDB; AAD02125.			
XX				
PT	Isolated TALL-1 protein is used to identify compounds that regulate B lymphocyte proliferation, used to treat B lymphocyte associated autoimmune disorders -			
XX				
PS	Claim 37: Page 104-105; 112pp: English.			
XX				
CC	The present invention relates to Tumour necrosis factor (TNF) and Apol-related leucocyte expressed Ligand 1 (TALL-1) nucleic acid molecules, proteins (including homologues), and their antibodies. The invention in particular relates to methods for regulating the interaction between TALL-1 and TALL-1 receptors (BCMA referred as B cell maturation factor) to regulate monocyte, macrophage and B lymphocyte mediated immune responses. TALL-1 protein is useful for identifying compounds that regulate B lymphocyte proliferation. It is also useful for treating B lymphocyte associated autoimmune disorders like rheumatoid arthritis, systemic lupus erythematosus (SLE), insulin dependent diabetes mellitus, multiple sclerosis, myasthenia gravis, Grave's disease, autoimmune haemolytic anaemia, autoimmune thrombocytopenia purpura, Goodpasture's syndrome, pemphigus vulgaris, acute rheumatic fever, post-streptococcal glomerulonephritis, or polyarteritis nodosa.			
CC	The TALL-1 protein and its corresponding nucleic acid sequence are also useful in diagnostic assays.			
CC	The present sequence is a human B cell maturation factor (BCMA) protein. It is the receptor for TALL-1 protein. BCMA gene is located on chromosome 16. In human tissues, BCMA is expressed by spleen and lymph nodes but not by brain, muscle, heart, lung, kidney, pancreas, testis and placenta. BCMA mRNA is absent in the pro-B lymphocyte stage but its expression increases with B lymphocyte maturation.			
CC				
XX				
SO	Sequence	184 AA:		
XX				
Query Match	100.0%;	Score 239; DB 22; Length 184;		
Best Local Similarity	100.0%;	Pred. No. 1,7e-21;		
Matches	42; Conservative	0; Mismatches	0; Gaps	0;
OY	1	MAGGCSONEKFFDLSILHACIPCOLRGSSNRPPLTCORYNASV	42	
DB	4	MAGGCSONEKFFDLSILHACIPCOLRGSSNRPPLTCORYNASV	45	
XX				
RESULT 9				
ID	ABB81487			
XX	ABB81487 standard; Protein; 184 AA.			
XX				
AC	ABB81487:			
XX				
DT	02-SEP-2002 (first entry)			
XX				

DE Human BCMA receptor related protein spq ID NO:7.

XX Human; ztnfr12; tumour necrosis factor receptor; cytostatic;
KW immunosuppressive; dermatological; antinflammatory; antidiabetic;
KW neuroprotective; antineumatic; antiarthritic; antiaustmatic;
KW neptrotropic; hypotensive; gene therapy; B lymphocyte; tumour;
KW autoimmune disorder; systemic lupus erythematosus; myasthenia gravis;
KW multiple sclerosis; insulin dependent diabetes mellitus; asthma;
KW rheumatoid arthritis; bronchitis; emphysema; renal disease; lymphoma;
KW glomerulonephritis; vasculitis; chronic lymphoid leukemia; nephritis;
KW pyelonephritis; renal neoplasia; multiple myeloma; amyloidosis;
KW light chain neuropathy; hypertension; large vessel disease;
KW graft-versus host disease; graft rejection; Crohn's disease.

XX Homo sapiens.

XX WO200238766-A2.

XX 16-MAY-2002.

XX 05-NOV-2001; 2001WO-US47018.

XX 07-NOV-2000; 2000US-24649P.

XX 20-DEC-2000; 2000US-25713P.

XX 28-JUN-2001; 2001US-301715P.

XX 29-AUG-2001; 2001US-315565P.

XX (ZYMO) ZYMOGENETICS INC.

XX Gross JA, Xu W, Henne RM, Grant FJ;

XX WPI; 2002-508212/54.

XX Novel isolated human tumor necrosis factor receptor polypeptide, termed

XX ztnfr 12, useful for treating autoimmune disorders, emphysema, end

XX stage renal failure or renal disease and Lymphoma

XX Disclosure: Page 135-136; 154pp; English.

XX The present invention describes a human tumour necrosis factor receptor

XX designated ztnfr12 (1), (1) has cytostatic, immunosuppressive,

XX dermatological, antinflammatory, neuroprotective, antidiabetic,

XX antirheumatic, antiarthritic, antiaustmatic, nephrotropic and hypotensive

XX activities, and can be used in gene therapy. (1) can be used for

XX inhibiting, in a mammal, the activity of a ligand that binds ztnfr12

XX (e.g. ztnfr4), for treating disorders and diseases associated with B

XX lymphocytes, activated B lymphocytes or resting B lymphocytes, and for

XX inhibiting the proliferation of tumour cells. (1) is useful for treating

XX autoimmune disorders such as systemic lupus erythematosus, myasthenia

XX gravis, multiple sclerosis, insulin dependent diabetes mellitus, asthma,

XX rheumatoid arthritis, bronchitis, emphysema and end stage renal failure

XX or renal disease such as glomerulonephritis, vasculitis, chronic lymphoid

XX leukaemia, nephritis, and pyelonephritis, and for treating renal

XX neoplasms, multiple myelomas, lymphomas, light chain neuropathy, or

XX amyloidosis, hypertension, large vessel diseases, graft-versus host

XX disease, graft rejection and Crohn's disease. (1) is useful for

XX modulating the immune system, for regulating B cell responses and

XX production, for modulating development of other cells, antibody

XX production and cytokine production, and for modulating T and B cell

XX communication. The present sequence represents a protein which is

XX given in the exemplification of the present invention.

XX Sequence 184 AA;

XX Query Match 100.0%; Score 239; DB 23; Length 184;

XX Best Local Similarity 100.0%; Pred. No. 1.7e-21;

XX Matches 42; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

RESULT 10

AAE15488 ID AAE15488 standard; Protein: 283 AA.

XX AAE15488;

XX 12-MAR-2002 (first entry)

XX Human BCMA-immunoglobulin Fc region fusion protein.

XX Human; transmembrane activator and intracellular CAML interactor; TAC1;

XX cytostatic; B cell maturation protein; BCMA; tumour necrosis factor; TNF;

XX lymphoproliferative disorder; tumour; lung; gastrointestinal; pancreatic;

XX prostate; inflammation; immune disorder; diarrhoea; psoriasis; colitis;

XX drug allergy; dermatitis; pneumonia; asthma; inflammatory bowel disease;

XX Crohn's disease; scleroderma; autoimmune disease; multiple sclerosis;

XX human immunodeficiency virus; HIV; systemic lupus erythematosus; cancer;

XX rheumatoid arthritis; atherosclerosis; fusion protein.

XX Homo sapiens.

XX WO200187979-A2.

XX 22-NOV-2001.

XX 14-MAY-2001; 2001WO-US15567.

XX 12-MAY-2000; 2000US-204039P.

XX 27-JUN-2000; 2000US-214591P.

XX 14-MAY-2001; 2001US-0214591.

XX (AMGE) AMGEN INC.

XX Theill LE, Yu G;

XX WPI; 2002-066686/09.

XX Inhibiting activity of B cell maturation protein and/or transmembrane

XX activator and intracellular cyclophilin ligand interactor, by

XX administering a binding partner for APRIL, a tumor necrosis factor

XX family ligand

XX Disclosure: Flg 10B; 94pp; English.

XX The invention relates to a method for inhibiting TAC1 (transmembrane

XX activator and intracellular CAML interactor) and/or B cell maturation

XX protein (BCMA) activity in a mammal. The method comprises administering

XX a specific binding partner for APRIL (G70, a tumour necrosis factor-TNF

XX family ligand), having the consensus sequence, but not the extracellular region

XX of TAC1 or BCMA. The method is useful for inhibiting activity of TAC1

XX and/or BCMA in a mammal which is useful for treating B-cell or T-cell

XX lymphoproliferative disorders, one or more solid tumours such as lung,

XX gastrointestinal, pancreatic or prostate tumour. APRIL, BCMA and TAC1

XX antagonists are useful for treating inflammation and immune function

XX diseases such as diarrhoea, psoriasis, allergies, pneumonia, atopic

XX dermatitis, respiratory allergic disease (asthma, hypersensitivity lung

XX disease), drug and insect sting allergy, inflammatory bowel disease

XX (Crohn's disease, colitis), scleroderma, autoimmune disease (multiple

XX sclerosis, rheumatoid arthritis, systemic lupus erythematosus), fungal,

XX bacterial, protozoal and viral infections (HIV), atherosclerosis, cancer

XX with leucocyte infiltration of the skin or organs. The present sequence

XX is human BCMA protein-immunoglobulin Fc region fusion protein.

XX Sequence 283 AA;

XX Query Match 100.0%; Score 239; DB 23; Length 283;

XX Best Local Similarity 100.0%; Pred. No. 2.6e-21;

XX Matches 42; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

XX 1 MAGCSQNEFYEDSLHACIPQALRCSSNTPPLTCORCNASV 42

XX 1 MAGCSQNEFYEDSLHACIPQALRCSSNTPPLTCORCNASV 42

XX 1 MAGCSQNEFYEDSLHACIPQALRCSSNTPPLTCORCNASV 42

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RESULT 11
AAE00507
ID AAE00507 standard; Protein; 302 AA.
XX
XX AAE00507;
XX
XX 31-JUL-2001 (first entry)
XX
XX
XX Human BCMA-Immunoglobulin G Fc region fusion construct.
XX
XX Human: A Proliferation Inducing Ligand Receptor; APRIL-R; cytostatic;
XX gene therapy; cancer; nephrotropic; renal disorder; autoimmune disease;
XX carcinoma; lung; colon; breast; prostate; Grave's disease; hypertension;
XX systemic lupus erythematosus; SLE; inflammation; cardiovascular disease;
XX B-cell lympho-proliferative disorder; BCM; immunosuppressive disease;
XX organ transplantation; HIV; human immunodeficiency virus; TNF; murine;
XX tumour necrosis factor; B cell maturation protein; BCMA; fusion protein;
XX immunoglobulin G; IgG; Fc region.
XX
XX Chimeric - Homo sapiens.
XX
XX Chimeric - Mus sp.
XX
XX Key
XX Location/Qualifiers
XX 1..22
XX /label= signal_peptide
XX /note= "Derived from murine Ig kappa sequence"
XX Protein
XX 23..302
XX /label= Mature_human_BCMA_IgG_Fc_fusion_protein
XX Region
XX 23..75
XX /note= "Derived from human BCMA protein"
XX Region
XX 76..302
XX /note= "Derived from human IgG Fc region"
XX Domain
XX 24..302
XX /label= Cysteine-rich_domain
XX /note= "Derived from human BCMA"
XX
XX MO200124811-A1.
XX
XX 12-APR-2001.
XX
XX 05-OCT-2000; 2000MO-US27579.
XX
XX 06-OCT-1999; 99US-0157933.
XX 11-FEB-2000; 2000US-0181807.
XX 30-JUN-2000; 2000US-0215688.
XX
XX (BIOJ ) BIOGEN INC.
XX (APOT-) APOTEC R & D SA.
XX
XX Schneider P, Thompson J, Cachero T, Ambrose C, Rennert P;
XX WPI; 2001-266242/27.
XX N-PSDB: AAD03847.
XX
XX Treating a mammal for a condition associated with undesired cell
XX proliferation such as cancer or carcinoma, comprises administering a
XX composition comprising a Proliferation Inducing Ligand Receptor
XX (APRIL-R) antagonist.
XX
XX Example 1: Fig 3B; 85pp; English.
XX
XX The invention relates to a method of treating a mammal for a condition
XX associated with undesired cell proliferation such as cancer or
XX carcinoma. The method involves administering a composition comprising
XX A Proliferation Inducing Ligand Receptor (APRIL-R) also referred as
XX B cell maturation protein (BCM or BCMA) antagonist that antagonises the
XX interaction between APRIL and its cognate receptor(s). This method is
XX useful for treating undesired cell proliferation such as cancer or
XX carcinoma e.g. human lung carcinoma, colon carcinoma, breast carcinoma,
XX prostate carcinoma, and other carcinomas whose proliferation is modulated
XX by APRIL. It is also useful for treating autoimmune diseases (Grave's

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CC disease, systemic lupus erythematosus (SLE); hypertension, cardiovascular
CC diseases, renal disorders, B-cell lympho-proliferative disorders,
CC immunosuppressive diseases, organ transplantation, inflammation and
CC human immunodeficiency virus (HIV), and for treating, suppressing or
CC altering an immune response involving a signalling pathway between
CC APRIL-R and its ligand. APRIL-R DNA is also useful in gene therapy.
CC The present sequence is a fusion construct containing human APRIL-R.
CC also referred as BCMA or BCM protein, Fc region of human immunoglobulin
CC G (196) and a signal sequence from murine Ig kappa cDNA.
XX
XX SQ Sequence 302 AA;
XX
XX Query Match 100.0%; Score 239; DB 22; Length 302;
XX Best Local Similarity 100.0%; Pred. No. 2,8e-21;
XX Matches 42; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX OY 1 MAGGCSQNEYFDLSLHACIPQALRCSSNTPPLTCQRYCNASV 42
XX |||||||
XX DB 27 MAGGCSQNEYFDLSLHACIPQALRCSSNTPPLTCQRYCNASV 68
XX
XX RESULT 12
XX AAB60699
XX ID AAB60699 standard; Protein; 302 AA.
XX
XX AC AAB60699;
XX
XX DT 22-MAY-2001 (first entry)
XX
XX Mouse IgG signal/human BAFF-R/human IgG Fc fusion protein, BAFF-R-Fc.
XX
XX Human BAFF-R: BAFF receptor; TNF family; immunoregulatory agent;
XX immune-related disorder; B-cell growth inhibitor;
XX B-cell maturation inhibitor; immunoglobulin production inhibitor;
XX autoimmune disorder; B-cell lymphoproliferative disorder; hypertension;
XX renal disorder; immunosuppressive disorder; HIV infection;
XX organ transplantation; antiinflammatory; systemic lupus erythematosus;
XX autoimmune haemolytic anaemia; Grave's disease; multiple myeloma;
XX B-cell carcinoma; leukaemia; rapidly progressive glomerulonephritis;
XX lymphoma; gene therapy; cancer; tumour; IgG Fc; fusion construct.
XX
XX Chimeric - Homo sapiens.
XX
XX Chimeric - Mus sp.
XX
XX MO200112812-A2.
XX
XX 22-FEB-2001.
XX
XX 16-AUG-2000; 2000MO-US22507.
XX 17-AUG-1999; 99US-0149378.
XX 11-FEB-2000; 2000US-0181684.
XX 18-FEB-2000; 2000US-0183536.
XX
XX (BIOJ ) BIOGEN INC.
XX (APOT-) APOTEC R & D SA.
XX
XX Mackay F, Browning J, Ambrose C, Tschopp J, Schneider P;
XX Thompson J;
XX WPI; 2001-202866/20.
XX N-PSDB: AAF59999.
XX
XX Inhibiting dendritic cell-induced B-cell growth, maturation and B-cell
XX lympho-proliferative disorder by administering BAFF-receptor
XX polypeptide, chimeric molecule comprising receptor or anti-BAFF-R
XX antibody homolog.
XX
XX Example 4; Fig 2; 59pp; English.
XX
XX The invention relates to the use of a BAFF receptor (BAFF-R, also known
XX as BCM) protein, or a BAFF-R fusion protein as an agent for the
XX treatment of a variety of immune-related disorders. BAFF-R is a member of

```

CC the TNF (tumour necrosis factor) family, acting as an immunoregulatory
CC agent, and also plays a role in the development of hypertension and
CC related disorders. BAF-R, fusion proteins containing it, and BAF-R-
CC specific antibodies can be used for inhibiting B-cell growth, dendritic
CC cell-induced B-cell growth and maturation, and immunoglobulin production,
CC and in the treatment of autoimmune disorders, B-cell lymphoproliferative
CC disorders, hypertension and renal disorders. The BAF-R proteins may also
CC be used in the treatment of immunosuppressive disorders and HIV
CC infection, and in patients undergoing organ transplantation. The BAF-R
CC proteins or BAF-R specific antibodies may be used for treating
CC suppressing or altering an immune response involving a signalling pathway
CC between BAF-R and BAF, thereby inhibiting inflammation. Since BAF-R
CC inhibits B-cell growth and maturation it is useful for treating diseases
CC such as systemic lupus erythematosus, autoimmune haemolytic anaemia,
CC grave's disease, multiple myeloma, B-cell carcinomas, leukaemia, rapidly
CC progressive glomerulonephritis, and lymphomas. Nucleic acids encoding
CC human BAF-R may be used in gene therapy to treat tumours, lymphomas,
CC autoimmune disorders and inherited B-cell-associated disorders. The
CC present sequence represents the BAF-R fusion protein BAF-R-Fc,
CC comprising a mouse IgG-kappa signal sequence, residues 1-153
CC of human BAF-R and a human IgG Fc sequence.
CC
CC
SQ Sequence 302 AA:

Query Match 100.0%; Score 239; DB 22; Length 302;
Best Local Similarity 100.0%; Pred. No. 2,8e-21;
Matches 42; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 MAGCGSQNEYFDSLHACIPCOLRCSSTNPPLTCORCNASV 42
Db 27 MAGCGSQNEYFDSLHACIPCOLRCSSTNPPLTCORCNASV 68
|||||

RESULT 13
AAEI5501
ID AAEI5501 standard; peptide: 58 AA.
AC AAEI5501;

DT 12-MAR-2002 (first entry)
XX
XX

DE Human B cell maturation protein cysteine rich extracellular region.

XX Human: transmembrane activator and intracellular CAML interactor; TACI;
KM cytostatic; B cell maturation protein; BCMA; tumour necrosis factor; TNF;
KM lymphoproliferative disorder; tumour; lung; gastrointestinal; pancreatic;
KM prostate; inflammation; immune disorder; diarrhoea; psoriasis; colitis;
KM drug allergy; dermatitis; pneumonia; asthma; inflammatory bowel disease;
KM Crohn's disease; scleroderma; autoimmune disease; multiple sclerosis;
KM human immunodeficiency virus; HIV; systemic lupus erythematosus; cancer;
KM rheumatoid arthritis; atherosclerosis.
XX
XX

OS Homo sapiens.
XX
PN WO200187979-A2.
XX

PD 22-NOV-2001.

PE 14-MAY-2001; 2001WO-US15567.

PR 12-MAY-2000; 2000US-20A039P.
PR 27-JUN-2000; 2000US-21A591P.
PR 14-MAY-2001; 2001US-021A591.

PA (AMGE-) AMGEN INC.

PI Theall LE, Yu G;

DR WPI: 2002-066686/09.

PT Inhibiting activity of B cell maturation protein and/or transmembrane
XX activator and intracellular cyclophilin ligand interactor. By
XX administering a binding partner for APRIL, a tumor necrosis factor

PT family ligand -
XX
XX Disclosure: Fig 13; 94pp; English.
PS

CC The invention relates to a method for inhibiting TACI (transmembrane
CC activator and intracellular CAML interactor) and/or B cell maturation
CC protein (BCMA) activity in a mammal. The method comprises administering
CC a specific binding partner for APRIL (970, a tumour necrosis factor-TNF
CC family ligand), having the consensus region of TACI, BCMA, or the TACI/
CC BCMA extracellular consensus sequence, but not the extracellular region
CC of TACI or BCMA. The method is useful for inhibiting activity of TACI
CC and/or BCMA in a mammal which is useful for treating B-cell or T-cell
CC lymphoproliferative disorders, one or more solid tumours such as lung,
CC gastrointestinal, pancreatic or prostate tumour, APRIL, BCMA and TACI
CC antagonists are useful for treating inflammation and immune function
CC diseases such as diarrhoea, psoriasis, allergies, pneumonia, atopic
CC dermatitis, respiratory allergic disease (asthma, hypersensitivity lung
CC disease), drug and insect sting allergy, inflammatory bowel disease
CC (Crohn's disease, colitis), scleroderma, autoimmune disease (multiple
CC sclerosis, rheumatoid arthritis, systemic lupus erythematosus), fungal,
CC bacterial, protozoal and viral infections (HIV), atherosclerosis, cancer
CC with leucocyte infiltration of the skin or organs. The present sequence
CC is human BCMA cysteine-rich extracellular region.
CC
CC
SQ Sequence 58 AA:

Query Match 91.6%; Score 219; DB 23; Length 58;
Best Local Similarity 100.0%; Pred. No. 1,4e-19;
Matches 38; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 5 CSONEYFDSLHACIPCOLRCSSTNPPLTCORCNASV 42
Db 1 CSONEYFDSLHACIPCOLRCSSTNPPLTCORCNASV 38
|||||

RESULT 14
AAEI5486
ID AAEI5486 standard; peptide: 34 AA.
AC AAEI5486;

DT 12-MAR-2002 (first entry)
XX
XX

DE Human B-cell maturation (BCMA) protein cysteine-rich consensus region.

XX Human: transmembrane activator and intracellular CAML interactor; TACI;
KM cytostatic; B cell maturation protein; BCMA; tumour necrosis factor; TNF;
KM lymphoproliferative disorder; tumour; lung; gastrointestinal; pancreatic;
KM prostate; inflammation; immune disorder; diarrhoea; psoriasis; colitis;
KM drug allergy; dermatitis; pneumonia; asthma; inflammatory bowel disease;
KM Crohn's disease; scleroderma; autoimmune disease; multiple sclerosis;
KM human immunodeficiency virus; HIV; systemic lupus erythematosus; cancer;
KM rheumatoid arthritis; atherosclerosis.
XX
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OS Homo sapiens.
XX
PN WO200187979-A2.
XX

PD 22-NOV-2001.

PE 14-MAY-2001; 2001WO-US15567.

PR 12-MAY-2000; 2000US-20A039P.
PR 27-JUN-2000; 2000US-21A591P.
PR 14-MAY-2001; 2001US-021A591.

PA (AMGE-) AMGEN INC.

PI Theall LE, Yu G;

DR WPI: 2002-066686/09.

PT Inhibiting activity of B cell maturation protein and/or transmembrane
XX activator and intracellular cyclophilin ligand interactor. By
XX administering a binding partner for APRIL, a tumor necrosis factor

PT activator and intracellular cyclophilin ligand interactor, by
administering a binding partner for APRIL, a tumor necrosis factor
family ligand -
XX
XX
Claim 1, Fig 10A; 94pp; English.

Claim 1; Fig 10A; 94pp; English.

The invention relates to a method for inhibiting TAC1 (transmembrane activator and intercellular CAM1 interactor) and/or B cell maturation protein (BCMA) activity in a mammal. The method comprises administering a specific binding partner for APRIL (G70, a tumour necrosis factor-TNF family ligand), having the consensus region of TAC1, BCMA, or the TAC1/BCMA extracellular consensus sequence, but not the extracellular region of TAC1 or BCMA. The method is useful for inhibiting a cell of TAC1 and/or BCMA in a mammal which is useful for treating B-cell or T-cell lymphoproliferative disorders, one or more solid tumours such as lung, gastrointestinal, pancreatic, or prostate tumour. APRIL, BCMA and TAC1 antagonists are useful for treating inflammation and immune function diseases such as dermatitis, psoriasis, allergies, pneumonia, atopic dermatitis, respiratory allergic disease (asthma), hypersensitivity lung disease), drug and insect stinging allergy, inflammatory bowel disease (Crohn's disease, colitis), scleroderma, autoimmune disease (multiple sclerosis, rheumatoid arthritis, systemic lupus erythematosus), fungal, bacterial, protozoal and viral infections (HIV, atherosclerosis), cancer with leucocyte infiltration of the skin or organs. The present sequence is human BCMA protein cysteine-rich consensus region.

SQ Sequence 34 AA;

Query Match	84.1%	Score 201;	DB 23;	Length 34;
Best Local Similarity	100.0%;	Pred. No. 1.3e-17;		
Matches	34;	Conservative	0;	Mismatches
			0;	Indels
				0;
				Gaps
				0;

```

Oy      5 CSQNEYFDSLHACIPQCLRCSNTPPLTCQRYC 38
         |||||
Db      1 CSQNEYFDSLHACIPQCLRCSNTPPLTCQRYC 34

```

RESULT 15
AAB60700

ID AAB60700 standard; protein; 157 aa.

AC AAB60700;

DT 22-MAY-2001 (first entry)

DE Human BAF² receptor (BAF²-R) sequence encoded by A plasmid pJST535

KW Human BAFF-R; BAFF receptor; TNF family; immunoregulatory agent;

KW B-cell maturation inhibitor; immunoglobulin production inhibitor;

KW renal disorder; immunosuppressive disorder; HIV infection;

KW autoimmune haemolytic anaemia; Grave's disease; multiple myeloma;

KW Lymphoma; gene therapy; cancer; tumour; plasmid pJST535.

05 Homo sapiens.

PN WO200112812-A

PD 22-FEB-2001.

16-AUG-2000;

PR 17-AUG-1999; 99US-0149378.

PR 18-FEB-2000; 2000US-0183536.

PA (BIOJ) BIOGEN INC.

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PI	Thompson J;
XX	
DR	WPI; 2001-202866/20
DR	N-PSDB; AAF60000.
XX	

PT Inhibiting dendritic

PT polypeptide, chimeric

PT Inhibiting dendritic cell-induced B-cell growth, maturation and B-cell
PT lympho-proliferative disorder by administering BAFF-receptor
PT polypeptide, chimeric molecule comprising receptor or anti-BAFF-R
PT antibody homolog -
XX
PS Example 1; Fig 3; 59pp. English.

Example 1; Fig 3; 59pp; English.

The invention relates to the use of a BAF β receptor (BAF β -R, also known as BCMA) protein, or a BAF β -R fusion protein as an agent for the treatment of a variety of immune-related disorders. BAF β -R is a member of the TNF (tumour necrosis factor) family, acting as an immunoregulatory agent, and also plays a role in the development of hypertension and related disorders. BAF β -R fusion proteins containing it, and BAF β -R specific antibodies can be used for inhibiting B-cell growth, dendritic cell-induced B-cell growth and maturation, and immunoglobulin production, and in the treatment of autoimmune disorders, B-cell lymphoproliferative disorders, hypertension and renal disorders. The BAF β -R proteins may also be used in the treatment of immunosuppressive disorders and HIV infection, and in patients undergoing organ transplantation. The BAF β -R protein, or BAF β -R specific antibodies may be used for treating, suppressing or altering an immune response involving a signalling pathway between BAF β -R and BAF β , thereby inhibiting inflammation. Since BAF β -R inhibits B-cell growth and maturation it is useful for treating diseases such as systemic lupus erythematosus, autoimmune haemolytic anaemia, Graves' disease, multiple myeloma, B-cell carcinomas, leukaemia, rapidly progressive glomerulonephritis, and lymphomas. Nucleic acids encoding human BAF β -R may be used in gene therapy to treat tumours, lymphomas, autoimmune disorders and inherited B-cell-associated disorders. The present sequence represents a human BAF β -R protein sequence as encoded by plasmid PJ5735. However, this BAF β -R protein sequence is 27 amino acids shorter than that given in AAB60698.

sq Sequence 157 AA;

every Match	75.7%;	Score 181;	DB 22;	Length 157;
1st Local Similarity	85.7%;	Pred. No. 1.7e-14;		
atches	35;	Conservative	0;	Mismatches 0;
				Indels 6;
				Gaps 2

QY I MAGCCSONEYFDLSLHACIPCQLRGSSNTPLTQRNCNASV 42
||| |||||||||||||||| ||||||||||||
Db 4 MAG--QNEYFDSLHACIPCQLR---NTPPLTCQRNCNASV 39

Search completed: November 12, 2002, 16:58:33
Job time : 17.0429 secs

GenCore version 5.1.3
Copyright (c) 1993 - 2002 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: November 12, 2002, 16:57:01 : Search time 5.76824 Seconds
(without alignments)
214.236 Million cell updates/sec

Title: US-09-848-271-2_COPY_4_45
Perfect score: 239

Sequence: 1 MAGOCSOMYFDSLHACIP.....LRCSSTPTTCORCYNASV 42

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 262574 seqs, 29422922 residues

Total number of hits satisfying chosen parameters: 262574

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents AA: *
1: /cgn2_6/ptodata/1/1aa/5A.COMB.pep: *
2: /cgn2_6/ptodata/1/1aa/5B.COMB.pep: *
3: /cgn2_6/ptodata/1/1aa/6A.COMB.pep: *
4: /cgn2_6/ptodata/1/1aa/6B.COMB.pep: *
5: /cgn2_6/ptodata/1/1aa/PCRTUS.COMB.pep: *
6: /cgn2_6/ptodata/1/1aa/Backfltest1.pep: *

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	67.5	28.2	166	2	US-08-810-572A-6 Sequence 6, Appl1
2	67.5	28.2	166	4	US-09-290-333-6 Sequence 4, Appl1
3	67.5	28.2	293	2	US-08-810-572A-2 Sequence 2, Appl1
4	67.5	28.2	293	4	US-09-290-333-2 Sequence 2, Appl1
5	56	23.4	2476	2	US-08-276-967-2 Sequence 2, Appl1
6	55.5	23.2	5405	2	US-08-718-388-9 Sequence 9, Appl1
7	54.5	22.8	350	2	US-08-999-811-4 Sequence 4, Appl1
8	54.5	22.8	350	2	US-08-824-996-2 Sequence 2, Appl1
9	54.5	22.8	350	3	US-09-042-105-4 Sequence 3, Appl1
10	54.5	22.8	350	4	US-08-510-133A-33 Sequence 33, Appl1
11	54.5	22.8	350	4	US-08-585-895-33 Sequence 3, Appl1
12	54.5	22.8	419	2	US-08-999-811-2 Sequence 2, Appl1
13	54.5	22.8	419	3	US-09-042-105-2 Sequence 18, Appl1
14	54.5	22.8	419	3	US-09-042-105-18 Sequence 8, Appl1
15	54.5	22.8	419	4	US-08-795-430-8 Sequence 35, Appl1
16	54.5	22.8	419	4	US-08-510-133A-35 Sequence 8, Appl1
17	54.5	22.8	419	4	US-09-355-700-8 Sequence 58, Appl1
18	54.5	22.8	419	4	US-09-355-700-58 Sequence 33, Appl1
19	54.5	22.8	419	4	US-08-601-133-33 Sequence 3, Appl1
20	54.5	22.8	419	4	US-08-706-058A-3 Sequence 2, Appl1
21	54.5	22.8	419	5	PCT-US96-09001-2 Sequence 3, Appl1
22	54	22.6	609	2	US-08-716-301-4 Sequence 4, Appl1
23	53.5	22.4	77	2	US-08-465-380-4 Sequence 4, Appl1
24	53.5	22.4	77	2	US-08-465-380-40 Sequence 40, Appl1
25	53.5	22.4	77	2	US-08-480-478-33 Sequence 33, Appl1
26	53.5	22.4	77	2	US-08-486-397-40 Sequence 40, Appl1
27	53.5	22.4	77	2	US-08-486-397-40 Sequence 40, Appl1

28	53.5	22.4	77	2	US-08-486-399-4 Sequence 4, Appl1
29	53.5	22.4	77	2	US-08-486-399-40 Sequence 40, Appl1
30	53.5	22.4	77	2	US-08-461-965-4 Sequence 4, Appl1
31	53.5	22.4	77	2	US-08-461-965-40 Sequence 40, Appl1
32	53.5	22.4	77	2	US-08-326-110A-33 Sequence 33, Appl1
33	53.5	22.4	77	2	US-08-634-641-4 Sequence 4, Appl1
34	53.5	22.4	77	2	US-08-634-641-40 Sequence 40, Appl1
35	53.5	22.4	77	3	US-09-249-471-4 Sequence 4, Appl1
36	53.5	22.4	77	3	US-09-249-471-40 Sequence 40, Appl1
37	53.5	22.4	77	3	US-09-249-472-40 Sequence 40, Appl1
38	53.5	22.4	77	3	US-09-249-472-40 Sequence 40, Appl1
39	53.5	22.4	77	3	US-09-249-451-4 Sequence 4, Appl1
40	53.5	22.4	77	3	US-08-809-455-40 Sequence 40, Appl1
41	53.5	22.4	77	3	US-08-809-455-40 Sequence 4, Appl1
42	53.5	22.4	77	3	US-09-249-461-40 Sequence 40, Appl1
43	53.5	22.4	77	3	US-09-249-461-40 Sequence 4, Appl1
44	53.5	22.4	77	3	US-09-249-461-40 Sequence 40, Appl1
45	53.5	22.4	77	3	US-09-249-448-4 Sequence 4, Appl1

ALIGNMENTS

RESULT 1
US-08-810-572A-6
Sequence 6, Application US/08810572A
Patent No. 5969102
GENERAL INFORMATION:
APPLICANT: Bram, Richard J.
TITLE OF INVENTION: A LYMPHOCYTE SURFACE RECEPTOR THAT BINDS
TITLE OF INVENTION: CAML, NUCLEIC ACIDS ENCODING THE SAME AND METHODS OF USE
NUMBER OF INVENTION: THEREOF
NUMBER OF SEQUENCES: 11
CORRESPONDENCE ADDRESSES:
ADDRESSEE: David A. Jackson, Esq.
STREET: 411 Hackensack Ave, Continental Plaza, 4th
CITY: Hackensack
STATE: New Jersey
COUNTRY: USA
ZIP: 07601
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/810,572A
FILING DATE: 28-FEB-1997
CLASSIFICATION: 536
ATTORNEY/AGENT INFORMATION:
NAME: Jackson Esq., David A.
REGISTRATION NUMBER: 26,742
REFERENCE/DOCKET NUMBER: 1340-1-007
TELECOMMUNICATION INFORMATION:
TELEPHONE: 201-487-5800
TELEFAX: 201-343-1684
INFORMATION FOR SEO ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 166 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
HYPOTHETICAL: NO
FRAGMENT TYPE: N-terminal
ORIGINAL SOURCE:
ORGANISM: Homo sapiens
US-08-810-572A-6
Query Match 28.2% Score 67.5; DB 2; Length 166;
Best Local Similarity 30.6%; Pred. No. 0.61;

Matches 11: Conservative 9; Mismatches 15; Indels 1; Gaps 1;

QY 5 CSQNEFDLSLHACIPQCLGSSNTPPTTCORICNA 40
1 : : 1 : 1 : 1 : 1 : 1 : 1 : 1 : 1 : 1 :
DB 34 CPEQYWDPLGTCMCKTICNHQS-ORTCAAFCRS 68

RESULT 2

US-09-290-333-6
Sequence 6, Application US/09290333

Patent No. 6316222

GENERAL INFORMATION:

APPLICANT: Bram, Richard J.

Von Bulow, Gotz

TITLE OF INVENTION: A LYMPHOCYTE SURFACE RECEPTOR THAT BINDS

CAML, NUCLEIC ACIDS ENCODING THE SAME AND METHODS OF USE

THEOREF

NUMBER OF SEQUENCES: 11

CORRESPONDENCE ADDRESS:

ADDRESSEE: David A. Jackson, Esq.

STREET: 411 Hackensack Ave, Continental Plaza, 4th

FLOOR

CITY: Hackensack

STATE: New Jersey

COUNTRY: USA

ZIP: 07601

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/290,333

FILING DATE: 12-Apr-1999

CLASSIFICATION: <Unknown>

ATTORNEY/AGENT INFORMATION:

NAME: Jackson Esq., David A.

REGISTRATION NUMBER: 26,742

REFERENCE/DOCKET NUMBER: 1340-1-007 PCT

TELECOMMUNICATION INFORMATION:

TELEPHONE: 201-487-5800

TELEFAX: 201-343-1684

INFORMATION FOR SEQ ID NO: 6:

SEQUENCE CHARACTERISTICS:

LENGTH: 166 amino acids

TYPE: amino acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: peptide

HYPOTHETICAL: NO

FRAGMENT TYPE: N-terminal

ORIGINAL SOURCE:

ORGANISM: Homo sapiens

SEQUENCE DESCRIPTION: SEQ ID NO: 6:

US-09-290-333-6

Query Match 28.2%; Score 67.5; DB 4; Length 166;

Best Local Similarity 30.6%; Pred. No. 0.61;

Matches 11; Conservative 9; Mismatches 15; Indels 1; Gaps 1;

QY 5 CSQNEFDLSLHACIPQCLGSSNTPPTTCORICNA 40
1 : : 1 : 1 : 1 : 1 : 1 : 1 : 1 : 1 : 1 :
DB 34 CPEQYWDPLGTCMCKTICNHQS-ORTCAAFCRS 68

RESULT 3

US-08-810-572A-2

Sequence 2, Application US/08810572A

Patent No. 5969102

GENERAL INFORMATION:

APPLICANT: Bram, Richard J.

Von Bulow, Gotz

TITLE OF INVENTION: A LYMPHOCYTE SURFACE RECEPTOR THAT BINDS

TITLE OF INVENTION: CAML, NUCLEIC ACIDS ENCODING THE SAME AND METHODS OF USE

THEOREF

NUMBER OF SEQUENCES: 11

CORRESPONDENCE ADDRESS:

ADDRESSEE: David A. Jackson, Esq.

STREET: 411 Hackensack Ave, Continental Plaza, 4th

FLOOR

CITY: Hackensack

STATE: New Jersey

COUNTRY: USA

ZIP: 07601

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/810,572A

FILING DATE: 28-FEB-1997

CLASSIFICATION: 536

ATTORNEY/AGENT INFORMATION:

NAME: Jackson Esq., David A.

REGISTRATION NUMBER: 26,742

REFERENCE/DOCKET NUMBER: 1340-1-007

TELECOMMUNICATION INFORMATION:

TELEPHONE: 201-487-5800

TELEFAX: 201-343-1684

INFORMATION FOR SEQ ID NO: 2:

SEQUENCE CHARACTERISTICS:

LENGTH: 293 amino acids

TYPE: amino acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: protein

HYPOTHETICAL: NO

FRAGMENT TYPE: N-terminal

ORIGINAL SOURCE:

ORGANISM: Homo sapiens

US-08-810-572A-2

Query Match 28.2%; Score 67.5; DB 2; Length 293;

Best Local Similarity 30.6%; Pred. No. 1.1;

Matches 11; Conservative 9; Mismatches 15; Indels 1; Gaps 1;

QY 5 CSQNEFDLSLHACIPQCLGSSNTPPTTCORICNA 40
1 : : 1 : 1 : 1 : 1 : 1 : 1 : 1 : 1 : 1 :
DB 34 CPEQYWDPLGTCMCKTICNHQS-ORTCAAFCRS 68

RESULT 4

US-09-290-333-2

Sequence 2, Application US/09290333

Patent No. 6316222

GENERAL INFORMATION:

APPLICANT: Bram, Richard J.

Von Bulow, Gotz

TITLE OF INVENTION: A LYMPHOCYTE SURFACE RECEPTOR THAT BINDS

CAML, NUCLEIC ACIDS ENCODING THE SAME AND METHODS OF USE

THEOREF

NUMBER OF SEQUENCES: 11

CORRESPONDENCE ADDRESS:

ADDRESSEE: David A. Jackson, Esq.

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CITY: Hackensack

STATE: New Jersey

COUNTRY: USA

ZIP: 07601

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MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.30

```

1      CURRENT APPLICATION DATA:
2      APPLICATION NUMBER: US/09/290,333
3      FILING DATE: 12-Apr-1999
4      CLASSIFICATION: <Unknown>
5      ATTORNEY/AGENT INFORMATION:
6      NAME: Jackson Esq., David A.
7      REGISTRATION NUMBER: 26,742
8      REFERENCE/DOCKET NUMBER: 1340-1-007 PCT
9      TELECOMMUNICATION INFORMATION:
10     TELEPHONE: 201-487-5800
11     TELEFAX: 201-343-1694
12     INFORMATION FOR SEQ ID NO: 2:
13     SEQUENCE CHARACTERISTICS:
14     LENGTH: 293 amino acids
15     TYPE: amino acid
16     STRANDEDNESS: single
17     TOPOLOGY: linear
18     MOLECULE TYPE: protein
19     HYPOTHETICAL: NO
20     FRAGMENT TYPE: N-terminal
21     ORIGINAL SOURCE:
22     ORGANISM: Homo sapiens
23     SEQUENCE DESCRIPTION: SEQ ID NO: 2:
24     US-09-290-333-2
25
26     Query Match          28.2%  Score 67.5; DB 4; Length 293;
27     Best Local Similarity 30.6%  Pred. No. 1.1;
28     Matches 11; Conservative 9; Mismatches 15; Indels 1; Gaps 1
29
30     QY 5 CSQNEFYDSLHACIPQLRCSSNTPPLTCORCYNA 40
31         1  : 1:1 11 1: 1: 1: 1: 1: 1: 1:
32     Db 34 CPBQYWDPLLTGCMSCRTICNHQS-QRTCAFCRS 68
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34     RESULT 5
35     US-08-276-967-2
36     Sequence 2, Application US/08276967
37     Patent No. 5851817
38     GENERAL INFORMATION:
39     APPLICANT: Hardy, Daniel M.
40     APPLICANT: Gardner, David L.
41     TITLE OF INVENTION: Species-Specific Egg-Binding Proteins of
42     TITLE OF INVENTION: Sperm
43     NUMBER OF SEQUENCES: 8
44     CORRESPONDENCE ADDRESS:
45     ADDRESSEE: Arnold, White & Durkee
46     STREET: P. O. Box 4433
47     CITY: Houston
48     STATE: Texas
49     COUNTRY: USA
50     ZIP: 77210-4433
51     COMPUTER READABLE FORM:
52     MEDIUM TYPE: floppy disk
53     COMPUTER: IBM PC compatible
54     OPERATING SYSTEM: PC-DOS/MS-DOS
55     SOFTWARE: PatentIn Release #1.0, Version #1.25
56     CURRENT APPLICATION DATA:
57     APPLICATION NUMBER: US/08/276,967
58     FILING DATE: Submitted Herewith
59     CLASSIFICATION: 530
60     ATTORNEY/AGENT INFORMATION:
61     NAME: Kitchell, Barbara S.
62     REGISTRATION NUMBER: 33,928
63     REFERENCE/DOCKET NUMBER: UTSID:418\KIT
64     TELECOMMUNICATION INFORMATION:
65     TELEPHONE: 713-787-1400
66     TELEFAX: 713-789-2679
67     TELEX: 79-0924
68     INFORMATION FOR SEQ ID NO: 2:
69     SEQUENCE CHARACTERISTICS:
70     LENGTH: 2476 amino acids
71     TYPE: amino acid
72     STRANDEDNESS: single

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      : TOPOLOGY: linear
      : MOLECULE TYPE: protein
      : US-08-276-967-2

Query Match                23.4%; Score 56; DB 2; Length 2476;
Best Local Similarity     31.6%; Pred. No. 1,9e+02;
Matches 12; Conservative   8; Mismatches 14; Indels 4; Gaps 2;

QY          5 CSONEYFDSLHACIP-CQ--LRCSNYPPLTCORYC 38
| | : | : | : | : | : | : | : | : | : | : | : | : |
Db 1851 CSAHSVYTSCVPSCPCLPSCQDPREGCTGAGARSTCEEGC 1888


RESULT 6
US-08-718-388-9
; Sequence 9, Application US/08718388
; Patent No. 6271362
; GENERAL INFORMATION:
APPLICANT: MORIKAWA, MINORU
APPLICANT: HORAKI, NAOKI
TITLE OF INVENTION: GENE ENCODING IGG Fc REGION-BINDING
TITLE OF INVENTION: PROTEIN
NUMBER OF SEQUENCES: 29
CORRESPONDENCE ADDRESSES:
ADDRESSEE: BIRCH, STEWART, KOLASCH AND BIRCH
STREET: PO BOX 747
CITY: FALLS CHURCH
STATE: VA
COUNTRY: USA
ZIP: 22040-0747

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/718,388
FILING DATE:
CLASSIFICATION: 536
ATTORNEY/AGENT INFORMATION:
NAME: MURPHY JR, GERALD M
REGISTRATION NUMBER: 28,977
REFERENCE/DOCKET NUMBER: 0230-111
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 205-8000
TELEFAX: (703) 205-8050
INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
LENGTH: 5405 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-718-388-9

Query Match                23.2%; Score 55.5; DB 4; Length 5405;
Best Local Similarity     33.3%; Pred. No. 4,7e+02;
Matches 12; Conservative   6; Mismatches 13; Indels 5; Gaps 2;

QY          4 QCSONEYFDSLHACIP-PCQLRCSNYPPLTCORYC 38
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Db 3933 ECPENSHYE---LCADTSLIGSGSAISNAFLQCPDSC 3964


RESULT 7
US-08-999-811-4
; Sequence 4, Application US/08999811
; Patent No. 5932540
; GENERAL INFORMATION:
APPLICANT: HU, JING-SHAN
APPLICANT: ROSEN, CRAIG A.
APPLICANT: CAO, LIANG
TITLE OF INVENTION: VASCULAR ENDOTHELIAL GROWTH FACTOR 2
NUMBER OF SEQUENCES: 15
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;; CORRESPONDENCE ADDRESS:
;; ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX
;; STREET: 1100 NEW YORK AVENUE
;; CITY: WASHINGTON
;; STATE: DC
;; COUNTRY: USA
;; ZIP: 20005
;;
;; COMPUTER READABLE FORM:
;; MEDIUM TYPE: Floppy disk
;; OPERATING SYSTEM: PC-DOS/MS-DOS
;; SOFTWARE: Patentin Release #1.0, Version #1.30
;;
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/08/999,811
;; FILING DATE: HEREMITH
;; CLASSIFICATION:
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: US 08/207,550
;; FILING DATE: 8-MAR-1994
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: US 08/465,968
;; FILING DATE: 06-JUN-1995
;; ATTORNEY/AGENT INFORMATION:
;; NAME: MARKOWICZ, KAREN R.
;; REGISTRATION NUMBER: 36,351
;; REFERENCE/DOCKET NUMBER: 1488.1000004
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: (202)371-2600
;; TELEFAX: (202)371-2540
;; INFORMATION FOR SEQ ID NO: 4:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 350 amino acids
;; TYPE: amino acid
;; TOPOLOGY: linear
;; MOLECULE TYPE: protein
;; US-08-999-811-4
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Query Match 22.8%; Score 54.5; DB 2; Length 350;
Best Local Similarity 35.0%; Pred. No. 41;
Matches 14; Conservative 2; Mismatches 21; Indels 3; Gaps 2;
;
Qy 4 OCSONEYFDSLHACIPQOLRCSSNTP--PLTCQRYCNAS 41
Db 258 OCGANREFDEMTCCV-CKRTCPRNQPLNPGKCAECCTES 296
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RESULT 8
US-08-824-996-2
; Sequence 2, Application US/08824996B
; Patent No. 5935820
; GENERAL INFORMATION:
; APPLICANT: Hu, Jing-Shan
; APPLICANT: Rosen, Craig A.
; TITLE OF INVENTION: Polynucleotides Encoding Vascular Endothelial Growth
; FILE REFERENCE: P112D1
; CURRENT APPLICATION NUMBER: US/08/824,996B
; CURRENT FILING DATE: 1997-03-27
; EARLIER APPLICATION NUMBER: 08/207,550
; EARLIER FILING DATE: 1994-03-08
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 2
; LENGTH: 350
; TYPE: PPT
; ORGANISM: Homo sapiens
US-08-824-996-2
;
Query Match 22.8%; Score 54.5; DB 2; Length 350;
Best Local Similarity 35.0%; Pred. No. 41;
Matches 14; Conservative 2; Mismatches 21; Indels 3; Gaps 2;

Qy 4 OCSONEYFDSLHACIPQOLRCSSNTP--PLTCQRYCNAS 41
Db 258 OCGANREFDEMTCCV-CKRTCPRNQPLNPGKCAECCTES 296
;
RESULT 9
US-09-042-105-4
; Sequence 4, Application US/09042105
; Patent No. 6040157
; GENERAL INFORMATION:
; APPLICANT: HU, JING-SHAN
; APPLICANT: ROSEN, CRAIG A.
; TITLE OF INVENTION: VASCULAR ENDOTHELIAL GROWTH FACTOR 2
; NUMBER OF SEQUENCES: 35
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX
; STREET: 1100 NEW YORK AVENUE
; CITY: WASHINGTON
; STATE: DC
; COUNTRY: USA
; ZIP: 20005
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/042,105
; FILING DATE: HEREMITH
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/207,550
; FILING DATE: 8-MAR-1994
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/465,968
; FILING DATE: 06-JUN-1995
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: TO BE ASSIGNED
; FILING DATE: 24-DEC-1997
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: ERIC K. STEFFE
; REGISTRATION NUMBER: 36,688
; REFERENCE/DOCKET NUMBER: 1488.1000003/EKS
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202)371-2540
; TELEFAX: (202)371-2600
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 350 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-09-042-105-4
;
Query Match 22.8%; Score 54.5; DB 3; Length 350;
Best Local Similarity 35.0%; Pred. No. 41;
Matches 14; Conservative 2; Mismatches 21; Indels 3; Gaps 2;
;
Qy 4 OCSONEYFDSLHACIPQOLRCSSNTP--PLTCQRYCNAS 41
Db 258 OCGANREFDEMTCCV-CKRTCPRNQPLNPGKCAECCTES 296
;
RESULT 10
US-08-510-133A-33
; Sequence 33, Application US/08510133A
; Patent No. 6221839
; GENERAL INFORMATION:
; APPLICANT: Alitalo, Kari

Joukov, Vladimir
TITLE OF INVENTION: Receptor Ligand
NUMBER OF SEQUENCES: 35
CORRESPONDENCE ADDRESS:
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
STREET: 6300 Sears Tower, 233 South Wacker Drive
CITY: Chicago
STATE: Illinois
COUNTRY: United States of America
ZIP: 60606-6402
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/510,133A
FILING DATE: 01-Aug-1995
CLASSIFICATION: <Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: Gass, David A.
REGISTRATION NUMBER: 38,153
REFERENCE/DOCKET NUMBER: 28113/32863
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312/474-6300
TELEFAX: 312/474-0448
TELEX: 25-3856
INFORMATION FOR SEQ ID NO: 33:
SEQUENCE CHARACTERISTICS:
LENGTH: 350 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 33:
US-08-510-133A-33
Query Match 22.8%; Score 54.5; DB 4; Length 350;
Best Local Similarity 35.0%; Pred. No. 41;
Matches 14; Conservative 2; Mismatches 21; Indels 3; Gaps 2;
OY 4 QCSONEYFDSLHACIPQCLRCSSNTP--PLTCORYCNAS 41
DB 258 QCGANREFDENTCQV-CKRTCPRNQPLNPKACBCTES 296
RESULT 11
US-08-585-895-33
Sequence 33; Application US/08585895
Patent No. 6245530
GENERAL INFORMATION:
APPLICANT: Allitalo, Karl
APPLICANT: Joukov, Vladimir
TITLE OF INVENTION: Receptor Ligand
NUMBER OF SEQUENCES: 35
CORRESPONDENCE ADDRESS:
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
STREET: 6300 Sears Tower, 233 South Wacker Drive
CITY: Chicago
STATE: Illinois
COUNTRY: United States of America
ZIP: 60606-6402
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/585,895
FILING DATE:
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: Gass, David A.
REGISTRATION NUMBER: 38,153

REFERENCE/DOCKET NUMBER: 28113/33072
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312/474-6300
TELEFAX: 312/474-0448
TELEX: 25-3856
INFORMATION FOR SEQ ID NO: 33:
SEQUENCE CHARACTERISTICS:
LENGTH: 350 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-585-895-33
Query Match 22.8%; Score 54.5; DB 4; Length 350;
Best Local Similarity 35.0%; Pred. No. 41;
Matches 14; Conservative 2; Mismatches 21; Indels 3; Gaps 2;
OY 4 QCSONEYFDSLHACIPQCLRCSSNTP--PLTCORYCNAS 41
DB 258 QCGANREFDENTCQV-CKRTCPRNQPLNPKACBCTES 296
RESULT 12
US-08-999-811-2
Sequence 2; Application US/08999811
Patent No. 5932540
GENERAL INFORMATION:
APPLICANT: HU, JING-SHAN
APPLICANT: ROSEN, CRAIG A.
APPLICANT: CAO, LIANG
TITLE OF INVENTION: VASCULAR ENDOTHELIAL GROWTH FACTOR 2
NUMBER OF SEQUENCES: 15
CORRESPONDENCE ADDRESS:
ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX
STREET: 1100 NEW YORK AVENUE
CITY: WASHINGTON
STATE: DC
COUNTRY: USA
ZIP: 20005
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/999,811
FILING DATE: HEREMITH
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/207,550
FILING DATE: 8-MAR-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/465,968
FILING DATE: 06-JUN-1995
ATTORNEY/AGENT INFORMATION:
NAME: MARKOWICZ, KAREN R.
REGISTRATION NUMBER: 36,351
REFERENCE/DOCKET NUMBER: 1488.1000004
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202)371-2600
TELEFAX: (202)371-2540
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 419 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-999-811-2
Query Match 22.8%; Score 54.5; DB 2; Length 419;
Best Local Similarity 35.0%; Pred. No. 49;
Matches 14; Conservative 2; Mismatches 21; Indels 3; Gaps 2;

OY 4 OCSQNEVFDLSLHACIPQOLRCSSNTP--PLTCQRYCNMS 41
DB 327 OCGANREFDENTCQCV-CKRTCPRNQPLNPGKCACTCTES 365

RESULT 13
US-09-042-105-2
Sequence 2, Application US/09042105
Patent No. 6040157
GENERAL INFORMATION:
APPLICANT: HU, JING-SHAN
APPLICANT: ROSEN, CRAIG A.
APPLICANT: CAO, LIANG
TITLE OF INVENTION: VASCULAR ENDOTHELIAL GROWTH FACTOR 2
NUMBER OF SEQUENCES: 35
CORRESPONDENCE ADDRESS:
ADDRESSEE: STERN, KESSLER, GOLDSTEIN & FOX
STREET: 1100 NEW YORK AVENUE
CITY: WASHINGTON
STATE: DC
COUNTRY: USA
ZIP: 20005
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/042,105
FILING DATE: HEREMITH
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/207,550
FILING DATE: 8-MAR-1994
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/465,968
FILING DATE: 06-JUN-1995
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: TO BE ASSIGNED
FILING DATE: 24-DEC-1997
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: ERIC K. STEFFE
REGISTRATION NUMBER: 36,688
REFERENCE/DOCKET NUMBER: 1488,1000003/EKS
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202)371-2600
TELEFAX: (202)371-2540
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 419 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-042-105-2

Query Match 22.8%; Score 54.5; DB 3; Length 419;
Best Local Similarity 35.0%; Pred. No. 49;
Matches 14; Conservative 2; Mismatches 21; Indels 3; Gaps 2;

OY 4 OCSQNEVFDLSLHACIPQOLRCSSNTP--PLTCQRYCNMS 41
DB 327 OCGANREFDENTCQCV-CKRTCPRNQPLNPGKCACTCTES 365

RESULT 14
US-09-042-105-18
Sequence 18, Application US/09042105
Patent No. 6040157
GENERAL INFORMATION:
APPLICANT: HU, JING-SHAN

APPLICANT: ROSEN, CRAIG A.
APPLICANT: CAO, LIANG
TITLE OF INVENTION: VASCULAR ENDOTHELIAL GROWTH FACTOR 2
NUMBER OF SEQUENCES: 35
CORRESPONDENCE ADDRESS:
ADDRESSEE: STERN, KESSLER, GOLDSTEIN & FOX
STREET: 1100 NEW YORK AVENUE
CITY: WASHINGTON
STATE: DC
COUNTRY: USA
ZIP: 20005
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/042,105
FILING DATE: HEREMITH
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/207,550
FILING DATE: 8-MAR-1994
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/465,968
FILING DATE: 06-JUN-1995
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: TO BE ASSIGNED
FILING DATE: 24-DEC-1997
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: ERIC K. STEFFE
REGISTRATION NUMBER: 36,688
REFERENCE/DOCKET NUMBER: 1488,1000003/EKS
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202)371-2600
TELEFAX: (202)371-2540
INFORMATION FOR SEQ ID NO: 18:
SEQUENCE CHARACTERISTICS:
LENGTH: 419 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-042-105-18

Query Match 22.8%; Score 54.5; DB 3; Length 419;
Best Local Similarity 35.0%; Pred. No. 49;
Matches 14; Conservative 2; Mismatches 21; Indels 3; Gaps 2;

OY 4 OCSQNEVFDLSLHACIPQOLRCSSNTP--PLTCQRYCNMS 41
DB 327 OCGANREFDENTCQCV-CKRTCPRNQPLNPGKCACTCTES 365

RESULT 15
US-08-795-430-8
Sequence 8, Application US/08795430
Patent No. 6130071
GENERAL INFORMATION:
APPLICANT: Altalo, Kari
APPLICANT: Joukov, Vladimir
TITLE OF INVENTION: Vascular Endothelial Growth Factor C (VEGF-C)
TITLE OF INVENTION: Protein and Gene, Mutants Thereof, and Uses Thereof
NUMBER OF SEQUENCES: 57
CORRESPONDENCE ADDRESS:
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
STREET: 6300 Sears Tower, 233 South Wacker Drive
CITY: Chicago
STATE: Illinois
COUNTRY: United States of America

ZIP: 60606-6402
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/795,430
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/FI96/00427
FILING DATE: 01-AUG-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/671,573
FILING DATE: 28-JUN-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/601,132
FILING DATE: 14-FEB-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/585,895
FILING DATE: 12-JAN-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/510,133
FILING DATE: 01-AUG-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/340,011
FILING DATE: 14-NOV-1994
ATTORNEY/AGENT INFORMATION:
NAME: Gass, David A.
REGISTRATION NUMBER: 38,153
REFERENCE/DOCKET NUMBER: 28967/33691
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312/474-6300
TELEFAX: 312/474-0448
TELEX: 25-3856
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 419 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-795-430-8

Query Match 22.8%; Score 54.5; DB 4; Length 419;
Best Local Similarity 35.0%; Pred. No. 49;
Matches 14; Conservative 2; Mismatches 21; Indels 3; Gaps 2;

OY 4 QCSQNEYFDLSLHACIFQALGCSNTP-PLTCORTGNMS 41
DB 327 QCGANREFDENTCQV-CKRTCPRNQPLNPGKCAECCTES 365

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Job time : 6.76824 secs

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OM protein - protein search, using sw model

Run on: November 12, 2002, 17:00:26 ; Search time 3.24464 Seconds

(without alignments)
186.640 Million cell updates/sec

Title: US-09-848-271-2_COPY_4_45

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Total number of hits satisfying chosen parameters: 92612

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications, AA:*

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3: /cgn2_6/ptodata/1/pubppaa/US06_NEW_PUB.pep:*
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14: /cgn2_6/ptodata/1/pubppaa/US60_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
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2	239	100.0	181	10	US-09-854-864-5
3	239	100.0	283	10	US-09-854-864-9
4	219	91.6	38	10	US-09-854-864-21
5	201	84.1	34	10	US-09-854-864-7
6	201	84.1	81	10	US-09-854-864-13
7	156	65.3	185	10	US-09-854-864-11
8	156	65.3	281	10	US-09-854-864-10
9	95.5	40.0	117	10	US-09-854-864-12
10	67.5	28.2	37	9	US-09-779-050A-43
11	67.5	28.2	59	10	US-09-854-864-20
12	67.5	28.2	166	10	US-09-854-864-15
13	67.5	28.2	291	9	US-09-779-050A-43
14	67.5	28.2	293	10	US-09-779-050A-43
15	67.5	28.2	293	10	US-09-879-919-22
16	67.5	28.2	293	10	US-09-854-864-14
17	67.5	28.2	293	10	US-09-854-864-14
18	67.5	28.2	397	10	US-09-854-864-18
19	66.5	27.8	67	10	US-09-854-864-16

20	64.5	27.0	418	9	US-09-886-429-2	Sequence 2, Appl1
21	64.5	27.0	735	10	US-09-898-570-10	Sequence 10, Appl
22	64.5	27.0	845	10	US-09-898-570-12	Sequence 12, Appl
23	64.5	27.0	974	10	US-09-898-570-14	Sequence 14, Appl
24	64.5	27.0	1009	10	US-09-898-570-16	Sequence 16, Appl
25	59.5	24.9	3034	10	US-09-737-149-25	Sequence 25, Appl
26	59.5	24.9	3034	10	US-09-737-149-25	Sequence 30, Appl
27	59	24.7	38	9	US-09-779-050A-46	Sequence 46, Appl
28	56	23.4	162	10	US-09-798-789-10	Sequence 10, Appl
29	55.5	23.2	5405	10	US-09-922-217-1116	Sequence 11, Ap
30	54.5	22.8	419	9	US-10-044-622-3	Sequence 3, Appl1
31	54.5	22.8	419	10	US-09-795-006A-22	Sequence 22, Appl
32	54.5	22.8	419	12	US-10-127-551-2	Sequence 2, Appl1
33	54.5	22.8	997	10	US-09-747-371-3	Sequence 3, Appl1
34	53	22.2	131	10	US-09-790-264-61	Sequence 61, Appl
35	52	21.8	689	10	US-09-071-838-2	Sequence 2, Appl
36	51.5	21.5	136	10	US-09-893-737-302	Sequence 302, App
37	51.5	21.5	392	10	US-09-898-570-39	Sequence 39, Appl
38	51.5	21.5	999	10	US-09-747-371-2	Sequence 2, Appl1
39	51	21.3	153	10	US-09-800-909-3	Sequence 3, Appl1
40	51	21.3	153	10	US-09-884-987-4	Sequence 4, Appl1
41	51	21.3	153	10	US-09-800-908-12	Sequence 12, Appl
42	51	21.3	161	9	US-09-898-234-4	Sequence 4, Appl1
43	51	21.3	161	10	US-09-899-422-4	Sequence 4, Appl1
44	51	21.3	161	10	US-09-907-263-2	Sequence 2, Appl1
45	51	21.3	162	10	US-09-798-789-9	Sequence 9, Appl1

ALIGNMENTS

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RESULT 1
US-09-854-864-6
; Sequence 6, Application US/09854864
; Patent No. US20020081296A1
; GENERAL INFORMATION:
; APPLICANT: THEILL, LARS EYDE
; APPLICANT: YU, GANG
; TITLE OF INVENTION: METHODS AND COMPOSITIONS OF MATTER CONCERNING APRIL/G70, BCMA
; FILE REFERENCE: A-686B
; CURRENT FILING DATE: 2001-09-11
; PRIOR APPLICATION NUMBER: US 60/204,039
; PRIOR FILING DATE: 2000-05-12
; PRIOR APPLICATION NUMBER: US 60/214,591
; NUMBER OF SEQ ID NOS: 31
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 6
; LENGTH: 51
; TYPE: PRP
; ORGANISM: Homo sapiens
US-09-854-864-6

Query Match          100.0%; Score 239; DB 10; Length 51;
Best Local Similarity 100.0%; Pred. No. 3.2e-22;
Matches 42; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 MAGGCSQNEYFDSLHACIPQLRSSNTPPLTCGRYCNASV 42
      |||
Db      1 MAGGCSQNEYFDSLHACIPQLRSSNTPPLTCGRYCNASV 42

RESULT 2
US-09-854-864-5
; Sequence 5, Application US/09854864
; Patent No. US20020081296A1
; GENERAL INFORMATION:
; APPLICANT: THEILL, LARS EYDE
; APPLICANT: YU, GANG
; TITLE OF INVENTION: METHODS AND COMPOSITIONS OF MATTER CONCERNING APRIL/G70, BCMA
; FILE REFERENCE: A-686B
; CURRENT FILING DATE: 2001-09-11
; PRIOR APPLICATION NUMBER: US 60/204,039
; PRIOR FILING DATE: 2000-05-12
; PRIOR APPLICATION NUMBER: US 60/214,591
; NUMBER OF SEQ ID NOS: 31
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 5
; LENGTH: 51
; TYPE: PRP
; ORGANISM: Homo sapiens
US-09-854-864-5
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; FILE REFERENCE: A-686B
; CURRENT APPLICATION NUMBER: US/09/854,864
; CURRENT FILING DATE: 2001-09-11
; PRIOR APPLICATION NUMBER: US 60/204,039
; PRIOR FILING DATE: 2000-05-12
; PRIOR APPLICATION NUMBER: US 60/214,591
; PRIOR FILING DATE: 2000-06-27
; NUMBER OF SEQ ID NOS: 31
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 5
; LENGTH: 181
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-854-864-5

Query Match          100.0%; Score 239; DB 10; Length 181;
Best Local Similarity 100.0%; Pred. No. 1,1e-21;
Matches 42; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 MAGGCSQNEFYDSLHACIPQCLRCSSNTPPLTCQRYCNASV 42
Db 1 MAGGCSQNEFYDSLHACIPQCLRCSSNTPPLTCQRYCNASV 42
|||||
RESULT 3
US-09-854-864-9
; Sequence 9, Application US/09854864
; Patent No. US20020081296A1
; GENERAL INFORMATION:
; APPLICANT: THEILL, LARS EYDE
; TITLE OF INVENTION: METHODS AND COMPOSITIONS OF MATTER CONCERNING APRIL/G70, BCMA,
; FILE REFERENCE: A-686B
; CURRENT APPLICATION NUMBER: US/09/854,864
; CURRENT FILING DATE: 2001-09-11
; PRIOR APPLICATION NUMBER: US 60/204,039
; PRIOR FILING DATE: 2000-05-12
; PRIOR APPLICATION NUMBER: US 60/214,591
; PRIOR FILING DATE: 2000-06-27
; NUMBER OF SEQ ID NOS: 31
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 9
; LENGTH: 283
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-854-864-9

Query Match          100.0%; Score 239; DB 10; Length 283;
Best Local Similarity 100.0%; Pred. No. 1,6e-21;
Matches 42; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 MAGGCSQNEFYDSLHACIPQCLRCSSNTPPLTCQRYCNASV 42
Db 1 MAGGCSQNEFYDSLHACIPQCLRCSSNTPPLTCQRYCNASV 42
|||||
RESULT 4
US-09-854-864-21
; Sequence 21, Application US/09854864
; Patent No. US20020081296A1
; GENERAL INFORMATION:
; APPLICANT: THEILL, LARS EYDE
; TITLE OF INVENTION: METHODS AND COMPOSITIONS OF MATTER CONCERNING APRIL/G70, BCMA,
; FILE REFERENCE: A-686B
; CURRENT APPLICATION NUMBER: US/09/854,864
; CURRENT FILING DATE: 2001-09-11
; PRIOR APPLICATION NUMBER: US 60/204,039
; PRIOR FILING DATE: 2000-05-12
; PRIOR APPLICATION NUMBER: US 60/214,591
; PRIOR FILING DATE: 2000-06-27
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; NUMBER OF SEQ ID NOS: 31
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 21
; LENGTH: 58
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-854-864-21

Query Match          91.6%; Score 219; DB 10; Length 58;
Best Local Similarity 100.0%; Pred. No. 8,4e-20;
Matches 38; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 5 CSQNEFYDSLHACIPQCLRCSSNTPPLTCQRYCNASV 42
Db 1 CSQNEFYDSLHACIPQCLRCSSNTPPLTCQRYCNASV 38
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RESULT 5
US-09-854-864-7
; Sequence 7, Application US/09854864
; Patent No. US20020081296A1
; GENERAL INFORMATION:
; APPLICANT: THEILL, LARS EYDE
; TITLE OF INVENTION: METHODS AND COMPOSITIONS OF MATTER CONCERNING APRIL/G70, BCMA,
; FILE REFERENCE: A-686B
; CURRENT APPLICATION NUMBER: US/09/854,864
; CURRENT FILING DATE: 2001-09-11
; PRIOR APPLICATION NUMBER: US 60/204,039
; PRIOR FILING DATE: 2000-05-12
; PRIOR APPLICATION NUMBER: US 60/214,591
; PRIOR FILING DATE: 2000-06-27
; NUMBER OF SEQ ID NOS: 31
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 7
; LENGTH: 34
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-854-864-7

Query Match          84.1%; Score 201; DB 10; Length 34;
Best Local Similarity 100.0%; Pred. No. 6,7e-18;
Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 5 CSQNEFYDSLHACIPQCLRCSSNTPPLTCQRYCNASV 38
Db 1 CSQNEFYDSLHACIPQCLRCSSNTPPLTCQRYCNASV 34
|||||
RESULT 6
US-09-854-864-13
; Sequence 13, Application US/09854864
; Patent No. US20020081296A1
; GENERAL INFORMATION:
; APPLICANT: THEILL, LARS EYDE
; TITLE OF INVENTION: METHODS AND COMPOSITIONS OF MATTER CONCERNING APRIL/G70, BCMA,
; FILE REFERENCE: A-686B
; CURRENT APPLICATION NUMBER: US/09/854,864
; CURRENT FILING DATE: 2001-09-11
; PRIOR APPLICATION NUMBER: US 60/204,039
; PRIOR FILING DATE: 2000-05-12
; PRIOR APPLICATION NUMBER: US 60/214,591
; PRIOR FILING DATE: 2000-06-27
; NUMBER OF SEQ ID NOS: 31
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 13
; LENGTH: 81
; TYPE: PRT
; ORGANISM: Consensus
US-09-854-864-13
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Query Match 84.1%; Score 201; DB 10; Length 81;
Best Local Similarity 100.0%; Pred. No. 1,3e-17;
Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 5 CSONEYFDSLHACIPCOLRCSSNTPPLTCORNC 38
|||||
DB 1 CSONEYFDSLHACIPCOLRCSSNTPPLTCORNC 34

RESULT 7
US-09-854-864-11
; Sequence 11, Application US/09854864
; Patent No. US20020081296A1
; GENERAL INFORMATION:
; APPLICANT: THEILL, LARS EYDE
; APPLICANT: YU, GANG
; TITLE OF INVENTION: METHODS AND COMPOSITIONS OF MATTER CONCERNING APRIL/G70, BCMA,
; FILE REFERENCE: A-686B
; CURRENT APPLICATION NUMBER: US/09/854,864
; CURRENT FILING DATE: 2001-09-11
; PRIOR APPLICATION NUMBER: US 60/204,039
; PRIOR FILING DATE: 2000-05-12
; PRIOR APPLICATION NUMBER: US 60/214,591
; PRIOR FILING DATE: 2000-06-27
; NUMBER OF SEQ ID NOS: 31
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 11
; LENGTH: 185
; TYPE: PRT
; ORGANISM: Murine
US-09-854-864-11

Query Match 65.3%; Score 156; DB 10; Length 185;
Best Local Similarity 69.0%; Pred. No. 7e-12;
Matches 29; Conservative 3; Mismatches 8; Indels 2; Gaps 1;

OY 1 MAGOCSONEYFDSLHACIPCOLRCSSNTPPLTCORNCASV 42
|||||
DB 1 MAOCFHSYFDSLHACIPCOLRCSSNTPPLTCORNCASV 40

RESULT 8
US-09-854-864-10
; Sequence 10, Application US/09854864
; Patent No. US20020081296A1
; GENERAL INFORMATION:
; APPLICANT: THEILL, LARS EYDE
; APPLICANT: YU, GANG
; TITLE OF INVENTION: METHODS AND COMPOSITIONS OF MATTER CONCERNING APRIL/G70, BCMA,
; FILE REFERENCE: A-686B
; CURRENT APPLICATION NUMBER: US/09/854,864
; CURRENT FILING DATE: 2001-09-11
; PRIOR APPLICATION NUMBER: US 60/204,039
; PRIOR FILING DATE: 2000-05-12
; PRIOR APPLICATION NUMBER: US 60/214,591
; PRIOR FILING DATE: 2000-06-27
; NUMBER OF SEQ ID NOS: 31
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 10
; LENGTH: 281
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-854-864-10

Query Match 65.3%; Score 156; DB 10; Length 281;
Best Local Similarity 69.0%; Pred. No. 1e-11;
Matches 29; Conservative 3; Mismatches 8; Indels 2; Gaps 1;
OY 1 MAGOCSONEYFDSLHACIPCOLRCSSNTPPLTCORNCASV 42
|||||

DB 1 MAOCFHSYFDSLHACIPCOLRCSSNTPPLTCORNCASV 40

RESULT 9
US-09-854-864-12
; Sequence 12, Application US/09854864
; Patent No. US20020081296A1
; GENERAL INFORMATION:
; APPLICANT: THEILL, LARS EYDE
; APPLICANT: YU, GANG
; TITLE OF INVENTION: METHODS AND COMPOSITIONS OF MATTER CONCERNING APRIL/G70, BCMA,
; FILE REFERENCE: A-686B
; CURRENT APPLICATION NUMBER: US/09/854,864
; CURRENT FILING DATE: 2001-09-11
; PRIOR APPLICATION NUMBER: US 60/204,039
; PRIOR FILING DATE: 2000-05-12
; PRIOR APPLICATION NUMBER: US 60/214,591
; PRIOR FILING DATE: 2000-06-27
; NUMBER OF SEQ ID NOS: 31
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 12
; LENGTH: 117
; TYPE: PRT
; ORGANISM: human-murine Consensus
US-09-854-864-12

Query Match 40.0%; Score 95.5; DB 10; Length 117;
Best Local Similarity 63.9%; Pred. No. 6.4e-05;
Matches 23; Conservative 3; Mismatches 3; Indels 7; Gaps 4;

OY 6 SONEYFDSLHACIPCOLRCSSNTPPLTCORNCASV 41
|||||
DB 2 AOCYFDSLHACIPCOLRCSSNTPPLTCORNCASV 30

RESULT 10
US-09-779-050A-45
; Sequence 45, Application US/09779050A
; Patent No. US20020160416A1
; GENERAL INFORMATION:
; APPLICANT: BOYLE, WILLIAM
; APPLICANT: HSU, HAILING
; TITLE OF INVENTION: RECEPTOR FROM TNF FAMILY
; FILE REFERENCE: A-570B
; CURRENT APPLICATION NUMBER: US/09/779,050A
; CURRENT FILING DATE: 2001-02-12
; PRIOR APPLICATION NUMBER: 60/181,800
; PRIOR FILING DATE: 2000-02-11
; NUMBER OF SEQ ID NOS: 52
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 45
; LENGTH: 37
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-779-050A-45

Query Match 28.2%; Score 67.5; DB 9; Length 37;
Best Local Similarity 30.6%; Pred. No. 0.044;
Matches 11; Conservative 9; Mismatches 15; Indels 1; Gaps 1;

OY 5 CSONEYFDSLHACIPCOLRCSSNTPPLTCORNCASV 40
|||||
DB 2 CPEBOYNDPLDTCMCKTICNMQS-ORICATACRS 36

RESULT 11
US-09-854-864-20
; Sequence 20, Application US/09854864
; Patent No. US20020081296A1
; GENERAL INFORMATION:
; APPLICANT: THEILL, LARS EYDE
; APPLICANT: YU, GANG

```

:
: TITLE OF INVENTION: METHODS AND COMPOSITIONS OF MATTER CONCERNING APRIL/570, BCMA
:
: TITLE OF INVENTION: PLYS/AGP-3, AND TACI
:
: FILE REFERENCE: A-686B
:
: CURRENT APPLICATION NUMBER: US/09/854,864
:
: CURRENT FILING DATE: 2001-09-11
:
: PRIOR APPLICATION NUMBER: US 60/204,039
:
: PRIOR FILING DATE: 2000-05-12
:
: PRIOR APPLICATION NUMBER: US 60/214,591
:
: PRIOR FILING DATE: 2000-06-27
:
: NUMBER OF SEQ ID NOS: 31
:
: SOFTWARE: PatentIn version 3.1
:
: SEQ ID NO 20
:
: LENGTH: 59
:
: TYPE: prt
:
: ORGANISM: Homo sapiens
:
: US-09-854-864-20

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Query Match	28.28;	Score 67.5;	DB 10;	Length 59;
Best Local Similarity	30.68;	Pred. No. 0.068;		
Matches 11; Conservative	9;	Mismatches 15;	Indels 1;	Gaps 1

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07      5 CSONEYPDSLHACIPQQLRCSSNTPLTQRCRMA 40
      | : : : | | : : : | : : : |
Db     1 CPEEQYMDPLLTGCMSCKTCNNQS-QRTCAACRCS 35

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RESULT 12
US-09-854-864-15

Patent No. US20020081296A1
GENERAL INFORMATION:
APPLICANT: THEILL, LARS EYDE

1 TITLE OF INVENTION: METHODS AND COMPOSITIONS OF MATTER CONCERNING APRIL/G70, BCMA
2
3 TITLE OF INVENTION: BLYS/AGP-3, AND TACI
4
5 FILE REFERENCE: A-686B
6

1 CURRENT FILING DATE: 2001-09-11
2
3 PRIORITY APPLICATION NUMBER: US 60/204,039
4
5 PRIORITY FILING DATE: 2000-05-12
6

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? SEQ_ID NO 13
? LENGTH: 166
? TYPE: PRT
? ORGANISM: Homo sapiens
?
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US-09-0034-004-13
Query Match      28.2%  Score 67.5;  DB 10;  Length 166;
Best Local Similarity
Pred. No. 0.18;

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Matches	11:	Conservative	9:	Mismatches	15:	Indels	1:	Gaps	1:
QY	5	CSONEYFDSLHACIPCOLRCSSNTPLTCORRYCA	40	:	:	:	:	:	:

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DB          34 CPEB01WDPPLG1TCSCKFTICNHOS-QRTICAFGRS 08
RESULT 13

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US-09-119-050A-43
: Sequence 43, Application US/09779050A
: Patent NO. US20020160416A1
: GENERAL INFORMATION:

APPLICANT: BOYLE, WILLIAM
APPLICANT: HSU, HAILING
TITLE OF INVENTION: RECEPTOR FROM TNF FAMILY
FILED NOVEMBER 9, 2006

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NUMBER OF SEQ ID NOS: 52

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: SOFTWARE: PatentIn version 3.0
: SEQ ID NO 43
:
: LENGTH: 291
:
: TYPE: PRT
:
: ORGANISM: Homo sapiens
:
US-03-779-050A-43

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Query Match	28.28;	Score 67.5;	DB 9;	Length 291;
Best local Similarity	30.68;	Pred. No. 0.31;		
Matches 11;	Conservative 9;	Mismatches 15;	Indels 1;	Gaps 1;

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Oy      5 CSQNEVFDLSLHACIPCOLRCSSNTPPLTCQRYCNA 40
         | : : : | | : : : | : : :
Db      34 CPSEQYWDPLGTGCMSCCTICNHQS-QRTCAAFCRS 68

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RESULT 14
US-09-779-050A-42

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;
;
; Patent NO. US20020160416A1
;
; GENERAL INFORMATION:
;
; APPLICANT: BOYLE, WILLIAM

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; TITLE OF INVENTION: RECEPTOR FROM THE FAMILY
 ; FILE REFERENCE: A-570B
 ; CURRENT APPLICATION NUMBER: US/09/779,050A

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; CONVENT FILING DATE: 2001-02-12
; PRIOR APPLICATION NUMBER: 60/181,800
; PRIOR FILING DATE: 2000-02-11
; NUMBER OF SEQ ID NOS: 52

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; SOFTWARE: EASYCNC VERSION 2.0
; SEQ ID NO 42
; LENGTH: 293
; TYPE: PRT

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	; ORGANISM: Homo sapiens	
	US-09-779-050A-42	
Query Match		28.28; Score 67.5; DB 9; Length 293;

5 CSONEYFDSLHACIPCOLRCSSNTPLTCORXCNA 40
Best Local Similarity 50.00; P-Id. No. 0.01;
Matches 11; Conservative 9; Mismatches 15; Indels 1; Gaps 1;

Db 34 CPEEQYMDPLIGTSCSKTICNHQS-QRTCAAFCRS 68

US-09-879-919-22
; Sequence 22, Application US/09879919
; Patent No. US20020064829A1

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: GENERAL INFORMATION:
: APPLICANT: Yu, Guo-Liang, et al.
: TITLE OF INVENTION: Human Tumor Necrosis Factor Delta and Epsilon
: FILE REFERENCE: BF253D1

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:
: CURRENT APPLICATION NUMBER: 05/09/879,919
:
: CURRENT FILING DATE: 2001-06-14
:
: PRIOR APPLICATION NUMBER: 60/293,499
:
: PRIOR FILING DATE: 2001-05-25
:

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; PRIOR APPLICATION NUMBER: 60/277,978
 ; PRIOR FILING DATE: 2001-03-23
 ; PRIOR APPLICATION NUMBER: 60/276,248
 ; PRIOR FILING DATE: 2001-03-16

; PRIOR APPLICATION NUMBER: 60/254,875
 ;
 ; PRIOR FILING DATE: 2000-12-13
 ;
 ; PRIOR APPLICATION NUMBER: 60/241,952
 ;
 ; PRIOR FILING DATE: 2000-10-23
 ;

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; PRIOR APPLICATION NUMBER: 60/211,537
;
; PRIOR FILING DATE: 2000-06-15
;
; PRIOR APPLICATION NUMBER: 08/815,783
;

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; PRIOR APPLICATION NUMBER: 60/016,812
; PRIOR FILING DATE: 1996-03-14
; NUMBER OF SEQ ID NOS: 26

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SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 22
LENGTH: 293
TYPE: PRT
ORGANISM: Homo sapiens
US-09-879-919-22

Query Match 28.2%; Score 67.5; DB 10; Length 293;
Best Local Similarity 30.6%; Pred. No. 0.31;
Matches 11; Conservative 9; Mismatches 15; Indels 1; Gaps 1;

QY 5 CSQNEYFDSLHACIPQQLRCSNTPPLTCQRYCNA 40
I : : I I I : : : : : : : : : : : :
Db 34 CPFEQYWDPLIGTCMSCKTICNHQS-QRTCAAFCRS 68

Search completed: November 12, 2002, 17:09:12
Job time : 3.24464 secs


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C:Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 21-Jan-2000
C:Accession: T25169
R:Wilkinson, J.
Submitted to the EMBL Data Library, October 1996
A:Reference number: Z19990
A:Accession: T25169
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-330 <TWI>
A:Cross-references: EMBL:Z81129; PIDN:CA03405.1; GSPDB:GN00023; CESP:T23P1.6
A:Experimental source: clone T23P1
C:Genetics:
A:Gene: CESP:T23P1.6
A:Map position: 5
A:Introns: 16/3
C:Superfamily: gliadin

Query Match          24.7%  Score 59;  DB 2;  Length 330;
Best Local Similarity 28.9%;  Pred. No. 13;
Matches 13;  Conservative 7;  Mismatches 17;  Indels 8;  Gaps 2;

OY      5  CSONEYFDSLHACIP-----COLRCSSNPPL--TCGRYCNAS 41
      1  : : : : : 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1
Db      59  CASSOYOLQTSOCMPACQOSCSOOCNTNTOCPTCOOSQCS 103
      1  : : : : : 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1

RESULT 8
T15577
Hypothetical protein C23G10.8 - Caenorhabditis elegans
C:Species: Caenorhabditis elegans
C:Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 21-Jan-2000
C:Accession: T15577
R:latreille, P.
Submitted to the EMBL Data Library, November 1995
A:Description: The sequence of C. elegans cosmid C23G10.
A:Reference number: Z18372
A:Accession: T15577
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-758 <LAT>
A:Cross-references: EMBL:U39851; NID:g1055062; PID:g105068; PIDN:AAA81069.1; CESP:C23G10.8
C:Genetics:
A:Gene: CESP:C23G10.8
A:Introns: 47/3; 237/3; 405/3; 487/1; 577/3; 694/3
C:Superfamily: Caenorhabditis elegans hypothetical protein C23G10.8

Query Match          24.7%  Score 59;  DB 2;  Length 758;
Best Local Similarity 42.9%;  Pred. No. 25;
Matches 9;  Conservative 6;  Mismatches 6;  Indels 0;  Gaps 0;

OY      12  DSLHACIPCOLRCSSNPPL 32
      1  : : 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1
Db      260  ESVFHPLYPAETRCSDCPPL 280

RESULT 9
A45558
epidermal growth factor receptor homolog precursor - fluke (Schistosoma mansoni)
N:contams: protein-tyrosine kinase (EC 2.7.1.112)
C:Species: Schistosoma mansoni
C:Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 10-Sep-1999
C:Accession: A45558; S27836
R:Shoemaker, C.B.; Ramachandran, H.; Landu, A.; dos Reis, M.G.; Stein, L.D.
Mol. Biochem. Parasitol. 53, 17-32, 1992
A>Title: Alternative splicing of the Schistosoma mansoni gene encoding a homologue of eg
A:Reference number: A45558; MUID:92365727; PMID:1501637
A:Accession: A45558
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-1717 <SMO>
A:Cross-references: EMBL:M86396; NID:g160957; PIDN:AA29866.1; PID:g160958
A>Note: sequence extracted from NCBI Backbone (NCBIP:111129)
C:Genetics:

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Oy      12 DCLHAC-IPQQLRC--SSNTPPLTCORYNAS 41
       || : | | | | | | | | | | | | | | |
Db      141 DSCQNVCNVCGGAGCAGYQNSPRAVCCQTGRGS 172

RESULT 12
AA3434

C:Superfamily: fluke epidermal growth factor receptor homolog 1; protein kinase homolo
C:Keywords: alternative splicing; ATP; autophosphorylation; glycoprotein; phosphoprot
F:1-19/Domains: signal sequence #status predicted <SIG>
F:20-1717/Product: epidermal growth factor receptor homolog 1 #status predicted <MAT>
F:1018-1323/Domains: protein kinase ATP-binding motif
F:1026-1034/Region: protein kinase ATP-binding motif

Query Match          24.7%; Score 59; DB 1; Length 1717;
Best Local Similarity 39.1%; Pred. No. 50;
Matches 9; Conservative 3; Mismatches 11; Indels 0; Gaps 0;

Oy      4 QCSONEYFDLHACIPQQLRCS 26
       :| :| | | | | | | | | |
Db      645 ECPNTYIDPQTRHCPCNESCS 667

RESULT 10
S07127
Chymotrypsin/elastase inhibitor - common roundworm
C:Species: Ascaris lumbricoles (common roundworm)
C:Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 24-Jul-1997
C:Accession: S07127
Arch. Biochem. Biophys. 232, 143-161, 1984
R:Babin, D.R.; Peansky, R.J.; Goos, S.M.
A>Title: The inhibitors of chymotrypsin/elastase from Ascaris lumbricoles: the pr
A:Reference number: S07127; MWID:84255715; PMID:6564898
A:Accession: S07127
A>Status: preliminary
A:Molecule type: protein
A:Residues: 1-63 <BAB>
C:Superfamily: roundworm trypsin inhibitor

Query Match          24.3%; Score 58; DB 2; Length 63;
Best Local Similarity 36.6%; Pred. No. 4; I;
Matches 15; Conservative 5; Mismatches 13; Indels 8; Gaps 4;

Oy      5 CSONEVFDSLHACIPQQLRC--SSNTP-PLTCOR-YCNAS 41
       || : | | | | | | | | | | | | | | |
Db      5 CGPNEVWTE---CTGCENKCGPDENTPCPLMKRRSPCECS 41

RESULT 11
T23681
Hypotheetical protein M02G9.1 - Caenorhabditis elegans
C:Species: Caenorhabditis elegans
C:Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999
C:Accession: T23681
R:Matthews, L.
Submitted to the EMBL Data Library, November 1996
A:Reference number: Z19781
A:Accession: T23681
A>Status: preliminary; translated from GB/EMBL/DDBU
A:Molecule type: DNA
A:Residues: 1-1513 <MI>
A:Cross-references: EMBL:Z81573; PIDN:CA804625.1; GSPDB:GN00020; CESP:M02G9.1
A:Experimental source: clone M02G9
C:Genetics:
A:Gene: CESP:M02G9.1
A:Map position: 2
A:Introns: 23/3; 71/3; 121/3; 183/1; 1083/3; 1141/3; 1408/1; 1449/1

Query Match          24.3%; Score 58; DB 2; Length 1513;
Best Local Similarity 43.8%; Pred. No. 59;
Matches 14; Conservative 3; Mismatches 13; Indels 2; Gaps 2;


```

furin (EC 3.4.21.75) 2 - fruit fly (*Drosophila melanogaster*)
 C:Species: *Drosophila melanogaster*
 C>Date: 04-Mar-1993 #sequence_revision 18-Nov-1994 #text_change 31-Mar-2000
 C:Accession: A43434
 R:Roedrock, A.J.; Creemers, J.W.; Pauli, I.G.; Kurzik-Dumke, U.; Reutrop, M.; Gateff, E.
 J. Biol. Chem. 267, 17208-17215, 1992
 A>Title: Cloning and functional expression of Dfurin2, a subtilisin-like proprotein proc
 A:Reference number: A43434; MUID:92381036; PMID:1512259
 A:Accession: A43434
 A:Status: preliminary
 A:Molecule type: mRNA
 A:Residues: 1-1680 <ROE>
 A:Cross-references: GB:M94375; NID:g157461; PID:g157462
 A>Note: sequence extracted from NCBI backbone (NCBIN:111933, NCBIPI:111934)
 C:Genetics:
 A:Gene: FLYBase:Fur2
 A:Cross-references: FLYBase:FBgn0004598
 C:Superfamily: subtilisin homology
 C:Keywords: hydrolase; serine proteolase; transmembrane protein
 F:409-657/Domain: subtilisin homology <SRT>
 F:418,457,638/Active site: Asp, His, Ser #status predicted

Query Match 24.18; Score 57.5; DB 2; Length 1680;
 Best Local Similarity 34.3%; Pred. No. 74;
 Matches 12; Conservative 5; Mismatches 17; Indels 1; Gaps 1;

OY 5 CSONEYFDSLHACIPOLRCS-NFPLTCORC 38
 DB 1199 GSESEFYSGVQCPCHASCSCNCPADTSC 1233

RESULT 13
 T20130
 hypothetical protein C50H2.3b - *Caenorhabditis elegans*
 C:Species: *Caenorhabditis elegans*
 C>Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999
 C:Accession: T20130
 R:McMurray, A.
 submitted to the EMBL Data Library, June 1996
 A:Reference number: 219226
 A:Accession: T20130
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: DNA
 A:Residues: 1-502 <MULT>
 A:Cross-references: EMBL:Z73971; PIDN:CAA98256.1; GSPDB:GN00023; CESP:C50H2.3b
 A:Experimental source: clone C50H2
 C:Genetics:
 A:Gene: CESP:C50H2.3b
 A:Map position: 5
 A:introns: 72/1; 122/1; 152/3; 188/1; 209/1; 255/1; 301/1; 339/1; 424/1

Query Match 23.88; Score 57; DB 2; Length 502;
 Best Local Similarity 34.7%; Pred. No. 31;
 Matches 17; Conservative 5; Mismatches 15; Indels 12; Gaps 3;

OY 1 MAGQSQNEFYDSLHACIPQL----RCSSNT----PELTCORYCNA 40
 DB 70 MNGQWQORYFD---HASTLCROFWMFDGCRSDSNIFDELTCOMICES 115

RESULT 14
 G96675
 hypothetical protein T23K8.9 [imported] - *Arabidopsis thaliana*
 C:Species: *Arabidopsis thaliana* (mouse-ear cress)
 C>Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 31-Mar-2001
 C:Accession: G96675
 R:Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso,
 Chlin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, K.;
 Hansen, N.F.; Hughes, B.; Hultzer, L.
 Nature 408, 816-820, 2000
 A:Authors: Hunter, J.U.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C.
 C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maiti, R.; Marziani,
 Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.

A:Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallo
 ker, M.; Wu, D.; Yu, G.; Fraser, C.W.; Venter, J.C.; Davis, R.W.
 A>Title: Sequence and analysis of chromosome 1 of the plant *Arabidopsis*.
 A:Reference number: A86141; MUID:21016719; PMID:11130712
 A:Accession: G96675
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-653 <STO>
 A:Cross-references: GB:AE005173; NID:g4646199; PIDN:AA026872.1; GSPDB:GN00141
 C:Genetics:
 A:Gene: T23K8.9
 A:Map position: 1

Query Match 23.88; Score 57; DB 2; Length 653;
 Best Local Similarity 38.9%; Pred. No. 38;
 Matches 14; Conservative 3; Mismatches 13; Indels 6; Gaps 2;

OY 3 GQCS--QNEFYDSLHACIPC----QLRCSNPNPL 32
 DB 194 GMSGLCGKIFDEMFHCSACNFTLDRCVSLPPL 229

RESULT 15
 T20125
 hypothetical protein C50H2.3a - *Caenorhabditis elegans*
 C:Species: *Caenorhabditis elegans*
 C>Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999
 C:Accession: T20125
 R:McMurray, A.
 submitted to the EMBL Data Library, June 1996
 A:Reference number: 219226
 A:Accession: T20125
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: DNA
 A:Residues: 1-838 <MULT>
 A:Cross-references: EMBL:Z73971; PIDN:CAA98251.1; GSPDB:GN00023; CESP:C50H2.3a
 A:Experimental source: clone C50H2
 C:Genetics:
 A:Gene: CESP:C50H2.3a
 A:Map position: 5
 A:introns: 31/1; 98/1; 162/1; 199/1; 244/1; 279/1; 323/1; 354/2; 391/1; 408/1; 458/1;

Query Match 23.88; Score 57; DB 2; Length 838;
 Best Local Similarity 34.7%; Pred. No. 47;
 Matches 17; Conservative 5; Mismatches 15; Indels 12; Gaps 3;

OY 1 MAGQSQNEFYDSLHACIPQL----RCSSNT----PELTCORYCNA 40
 DB 406 MNGQWQORYFD---HASTLCROFWMFDGCRSDSNIFDELTCOMICES 451

Search completed: November 12, 2002, 17:01:04
 Job time : 8.48927 secs

GenCore version 5.1.3
Copyright (c) 1993 - 2002 Compugen Ltd.

OM protein - protein search, using sw model

Run on: November 12, 2002, 16:49:26 ; Search time 3.60515 Seconds
(without alignments)
483,199 Million cell updates/sec

Title: US-09-848-271-2_COPY_4_45
Perfect score: 239
Sequence: 1 MAGCSCQNEFYDSLHACIP.....LMRCSSNPPLTCRCRYCNASV 42

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 112892 seqs, 41476328 residues

Total number of hits satisfying chosen parameters: 112892

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SWISSPROT_40:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	239	100.0	184	TR17_HUMAN	Q02223 homo sapien
2	156	65.3	185	TR17_MOUSE	086472 mus musculu
3	71.5	29.9	249	TI1X_MOUSE	096735 mus musculu
4	69.5	29.1	1877	PKC3_MOUSE	004592 mus musculu
5	69.5	29.1	5376	ZAN_MOUSE	086799 mus musculu
6	67.5	28.2	293	TI1X_HUMAN	014836 homo sapien
7	63	26.4	175	TI1C_MOUSE	0948d0 mus musculu
8	62	25.9	1592	SORL_CHICK	099930 g. sortilin-
9	60	25.1	867	SSPO_BOVIN	P38167 bos taurus
10	59.5	24.3	3024	CLRL_MOUSE	035161 mus musculu
11	58	24.3	63	ICE1_ASCSV	P07851 ascaris suu
12	57.5	24.1	1680	FUR2_DROME	P30432 drosophila
13	57	23.8	708	YB40_HUMAN	Q9ult0 homo sapien
14	56.5	23.6	99	GAS3_ARATH	P46687 arabidopsis
15	56	23.4	2476	ZAN_PIG	028983 sus scrofa
16	55	23.0	760	E2_DROME	P42124 drosophila
17	54.5	22.8	419	VEGC_HUMAN	P49767 homo sapien
18	54	22.6	1980	MY9B_RAT	063358 rattus norv
19	54	22.6	2114	MY9B_MOUSE	09qy06 mus musculu
20	54	22.6	2158	MY9B_HUMAN	013459 homo sapien
21	53.5	22.4	381	P53_CANFA	Q02937 canis famli
22	53.5	22.4	758	YJ06_YEAST	P39929 saccharomyc
23	53	22.2	131	ALK1_MOUSE	P97330 mus musculu
24	53	22.2	591	KPC2_RABIT	019111 oryctolagus
25	53	22.2	592	KPC2_MOUSE	002056 mus musculu
26	52.5	22.0	323	TNR6_BOVIN	P51867 bos taurus
27	52.5	22.0	847	TNR6_PYYAC	Q06670 autographa
28	52	21.8	56	ITR4_RADMA	028644 radianthus
29	52	21.8	304	TFPI_MACMU	Q28654 macaca mula
30	52	21.8	470	PROP_CAVPO	064181 cavia porce
31	52	21.8	1483	UFDA_YEAST	P33302 saccharomyc
32	52	21.8	1696	PKC5_BRACL	090115 brachiost
33	51.5	21.5	63	AMP2_MIRAJ	P25404 mirabilis j

ALIGNMENTS

RESULT 1	TR17_HUMAN	STANDARD:	PRT:	184 AA.
ID	TR17_HUMAN			
AC	Q02223;			
DT	01-JUL-1993 (Rel. 26, Created)			
DT	01-JUL-1993 (Rel. 26, Last sequence update)			
DT	15-JUN-2002 (Rel. 41, Last annotation update)			
DE	Tumor necrosis factor receptor superfamily member 17 (B-cell maturation protein).			
GN	TNFRSF17 OR BCM4 OR BCM.			
OS	Homo sapiens (Human).			
OC	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.			
OX	NCBI_TaxID=9606;			
RN	[1]			
RP	SEQUENCE FROM N.A., AND CHROMOSOMAL TRANSLOCATION.			
RC	TISSUE=peripheral blood leukocytes, and Lymph node;			
RC	MEDLINE=93010984; PubMed=1396583;			
RA	Laabi Y., Gras M.P., Carbonnel F., Brouet J.C., Berger R., Larsen C.J., Tsapis A.;			
RT	"A new gene, BCM, on chromosome 16 is fused to the interleukin 2 gene by a t(4;16)(q26;p13) translocation in a malignant T cell lymphoma.";			
RL	EMBO J. 11:3897-3904(1992).			
RN	[2]			
RP	SEQUENCE FROM N.A.			
RC	MEDLINE=94218235; PubMed=8165126;			
RA	Laabi Y., Gras M.P., Brouet J.C., Berger R., Larsen C.J., Tsapis A.;			
RT	"The BCM4 gene, preferentially expressed during B lymphoid maturation, is bidirectionally transcribed.";			
RL	Nucleic Acids Res. 22:1147-1154(1994).			
RN	[3]			
RP	SEQUENCE FROM N.A.			
RC	MEDLINE=94425270; PubMed=10493829;			
RA	Loftus B.J., Kim U.-J., Sneddon V.P., Kalush F., Brandon R., Fuhrman J., Mason T., Crosby M.L., Barnstead M., Cronin L., Deslattes Mays A., Cao Y., Xu R.X., Kang H.-L., Mitchell S., Eichler E.E., Harris P.C., Venter J.C., Adams M.D.;			
RT	"Genome duplications and other features in 12 Mb of DNA sequence from human chromosome 16p and 16q.";			
RL	Genomics 60:295-308(1999).			
RN	[4]			
RP	SEQUENCE FROM N.A., AND VARIANT THR-153.			
RC	MEDLINE=21419161; PubMed=11528522;			
RA	Kawasaki A., Tsuchiya N., Fukazawa T., Hashimoto H., Tokunaga K.;			
RT	"Presence of four major haplotypes in human BCM4 gene: lack of association with systemic lupus erythematosus and Rheumatoid arthritis.";			
RL	Genes Immun. 2:276-279(2001).			
RN	[5]			
RP	FUNCTION.			
RC	MEDLINE=20363816; PubMed=10903733;			
RA	Hatzoglou A., Roussel J., Bourgeade M.-F., Rogier E., Madry C., Inoue J., Devergne O., Tsapis A.;			
RT	"TNF receptor family member BCM4 (B cell maturation) associates with TNF receptor-associated factor (TRAF) 1, TRAF2, and TRAF3 and activates NF-kappa B, elk-1, C-Jun N-terminal kinase, and p38			

34 51.5 21.5 701 1 YAB5_SCHPO 009807 schizosacch
35 51.5 21.5 1935 1 YBBA_SCHPO 060072 schizosacch
36 51.5 21.5 3695 1 LMA5_HUMAN 015230 homo sapien
37 51 21.3 183 1 Y189_ACISP 0935x7 actinobact
38 51 21.3 455 1 TRIA_HUMAN P19438 homo sapien
39 51 21.3 592 1 KPC2_RAT P09217 rattus norv
40 51 21.3 1062 1 NAL2_HUMAN 09nx02 homo sapien
41 51 21.3 3718 1 LMA5_MOUSE 061001 mus musculu
42 50.5 21.1 100 1 KR22_COLLI 093499 columba liv
43 50.5 21.1 610 1 C4BP_BOVIN 028065 bos taurus
44 50.5 21.1 1013 1 PRML_DROME P82295 drosophila
45 50.5 21.1 3014 1 CLRL_HUMAN 09ny96 homo sapien

RT mltogen-activated protein kinase.";
 RL J. Immunol. 165:1322-1330(2000).
 RN [6]
 RP FUNCTION.
 RX MEDLINE:20259066; PubMed-10801128;
 RA Gross J.A., Johnston J., Mudri S., Enselman R., Dillon S.R.,
 RA Madden K., Xu W., Parrish-Novak J., Foster D., Lofton-Day C.,
 RA Moore M., Litlau A., Grossman A., Haugen H., Foley K., Blumberg H.,
 RA Harrison K., Kinsvogel W., Clegg C.H.;
 RT "TACI and BCMA are receptors for a TNF homologue implicated in B-cell
 RT autoimmune disease";
 RL Nature 404:995-999(2000).
 RN [7]
 RP FUNCTION, AND INTERACTION WITH APRIL AND BAFF.
 RX MEDLINE:21170294; PubMed-10973284;
 RA Yu G., Boone T., Delaney J., Hawkins N., Kelley M., Ramakrishnan M.,
 RA McCabe S., Qiu W.R., Kornum M., Xia X.-Z., Guo J., Stolina M.,
 RA Boyle W.J., Sarosi I., Hsu H., Senaldi G., Trell L.F.;
 RT "APRIL and TRAF1 and receptors BCMA and TACI: system for regulating
 RT humoral immunity";
 RL Nat. Immunol. 1:252-256(2000).
 RN [8]
 RP INTERACTION WITH TRAF5 AND TRAF6.
 RX MEDLINE:20381353; PubMed-10908663;
 RA Shu H.-B., Johnson H.;
 RT "B cell maturation protein is a receptor for the tumor necrosis factor
 RT family member TRAF1";
 RL Proc. Natl. Acad. Sci. U.S.A. 97:9156-9161(2000).
 CC -1- FUNCTION: Receptor for TNFSF13B/BAFF and TNFSF13/APRIL.
 CC Promotes B-cell survival and plays a role in the regulation of
 CC humoral immunity. Activates NF-kappa-B and JNK.
 CC -1- SUBUNIT: Associates with TRAF1, TRAF2, TRAF3, TRAF5 and TRAF6.
 CC -1- SUBCELLULAR LOCATION: Type III membrane protein. Plasma membrane
 CC and perinuclear Golgi-like structures.
 CC -1- TISSUE SPECIFICITY: Expressed in mature B-cells, but not in T-
 CC cells or monocytes.
 CC -1- DISEASE: A FORM OF T-CELL ACUTE LYMPHOBLASTIC LEUKEMIA (T-ALL) IS
 CC CHARACTERIZED BY A CHROMOSOMAL TRANSLOCATION t(4;16)(Q26;p13)
 CC WHICH INVOLVES BCMA AND IL2.
 CC -1- SIMILARITY: CONTAINS 1 TNFR-CYS REPEAT.
 CC -----
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 CC -----
 CC EMBL: 214954; CAA78679.1; -
 CC EMBL: 229575; CAA82691.1; -
 CC EMBL: 229574; CAA82690.1; -
 CC EMBL: U95742; AAB67251.1; -
 CC EMBL: AB05772; BAB60895.1; -
 CC PIR: S31208; S31208.
 CC PIR: S31209; S31209.
 CC Genew: HGNC:11913; TNFRSF17.
 DR MIM: 109545; -
 KW Receptor; Immune response; Proto-oncogene; Signal-anchor;
 KM Transmembrane; Chromosomal translocation; Polymorphism;
 FT DOMAIN 1 54
 FT TRANSMEM 55 77
 FT SIGNAL-ANCHOR (TYPE III MEMBRANE PROTEIN)
 FT (POTENTIAL).
 FT DOMAIN 78 184
 FT REPEAT 7 41
 FT SITE 3 4
 FT TNFR-CYS.
 FT BREAKPOINT FOR TRANSLOCATION TO FORM
 FT INTERLEUKIN 2/BCM ONCOGENE.
 FT DISULFID 8 21
 FT DISULFID 24 37
 FT DISULFID 28 41
 FT VARIANT 153 153
 FT A->T.
 FT /FTID=VAR_012234.
 SQ SEQUENCE 184 AA; 20138 MW; 277AF1E2767D932 CRC64;

Query Match 100.0%; Score 239; DB 1; Length 184;
 Best Local Similarity 100.0%; Pred. No. 1e-22;
 Matches 42; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Oy 1 MAGCCSQNEYFDSLHACIPCOLRCSSNTPPTTCORCVASV 42
 Db 4 MAGCCSQNEYFDSLHACIPCOLRCSSNTPPTTCORCVASV 45
 RESULT 2
 TR17_MOUSE
 ID TR17_MOUSE STANDARD: PRT; 185 AA.
 AC 088472;
 DT 15-JUN-2002 (Rel. 41, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Tumor necrosis factor receptor superfamily member 17 (B-cell
 DE maturation protein). BCM.
 GN TNFSF17 OR BCMA OR BCM.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_Taxid=10090;
 RN [1]
 RP SEQUENCE FROM N.A. (ISOFORMS 1 AND 2).
 RC STRAIN=BAIB/c; TISSUE=Spleen.
 RX MEDLINE:99061155; PubMed-984698;
 RA Madry C., Laabi Y., Callebaut I., Roussel J., Hatzoglou A.,
 RA Le Coniat M., Morion J.P., Berger R., Tsapis A.;
 RT "The characterization of murine BCMA gene defines it as a new member
 RT of the tumor necrosis factor receptor superfamily";
 RL Int. Immunol. 10:1693-1702(1998).
 RN [2]
 RP SEQUENCE FROM N.A. (ISOFORM 1).
 RC STRAIN=C57BL/6J; TISSUE=Colon.
 RX MEDLINE:21085660; PubMed-11217851;
 RA Kawai J., Shunagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
 RA Arakawa T., Hara A., Fukunishi Y., Kono H., Adachi J., Fukuda S.,
 RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamataka I.,
 RA Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
 RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
 RA Fleischmann W., Gaasterland T., Glisic C., King B., Kochia H.,
 RA Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
 RA Schiml L.M., Steubli F., Suzuki R., Tomita M., Wagner L., Yasuno T.,
 RA Sakai K., Okido T., Furuno M., Aono H., Balderelli R., Barsh G.,
 RA Blake J., Bottelli D., Bojunga N., Carlini P., de Bonaudo M.F.,
 RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
 RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
 RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,
 RA Norone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
 RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
 RA Suzuki H., Toyooka K., Wang K.H., Weltz C., Whitaker C., Winking L.,
 RA Wyszynski B., Yoshida K., Hasegawa Y., Kawai H., Kohlski S.,
 RA Hayashizaki Y.;
 RT "Functional annotation of a full-length mouse cDNA collection";
 RL Nature 409:685-690(2001).
 CC -1- FUNCTION: Receptor for TNFSF13B/BAFF and TNFSF13/APRIL.
 CC Promotes B-cell survival and plays a role in the regulation of
 CC humoral immunity. Activates NF-kappa-B and JNK (by similarity).
 CC -1- SUBUNIT: Associates with TRAF1, TRAF2, TRAF3, TRAF5 and TRAF6 (by
 CC similarity).
 CC -1- SUBCELLULAR LOCATION: Type III membrane protein (Probable).
 CC -1- ALTERNATIVE PRODUCTS: 2 isoforms; 1 (shown here) and 2; are
 CC produced by alternative splicing.
 CC -1- TISSUE SPECIFICITY: Detected in spleen, thymus, bone marrow and
 CC heart, and at lower levels in kidney and lung.
 CC -1- SIMILARITY: CONTAINS 1 TNFR-CYS REPEAT.
 CC -----
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 CC -----
 DR EMBL: AF061505; AAC23799.1; -
 DR EMBL: AK020247; BAB32038.1; -
 DR MGD: MGI:1343050; Tnftrsf17.
 KW Receptor; Immune response; Signal-anchor; Transmembrane;
 KM Alternative splicing.
 FT DOMAIN 1 49
 FT TRANSMEM 50 70
 FT
 FT DOMAIN 71 185
 FT REPEAT 4 36
 FT DISULFID 5 18
 FT DISULFID 21 32
 FT DISULFID 25 36
 FT VARSPLIC 87 91
 FT SEQUENCE 185 AA; 20442 MW; 8806352B4FD26A8F CRC64;
 SO
 Query Match 65.3%; Score 156; DB 1; Length 185;
 Best Local Similarity 69.0%; Pred. No. 1.7e-12;
 Matches 29; Conservative 3; Mismatches 8; Indels 2; Gaps 1;
 QY 1 MAGCSONEYFDSLHACIPQLNCSSNTPPLTCORCNAV 42
 DB 1 MAQCSEHSEYFDSLHACIPQLNCSSNTPPLTCORCNAV 40
 RESULT 3
 T13X_MOUSE STANDARD; PRT; 249 AA.
 ID T13X_MOUSE
 AC Q9ET35; Q9DB23;
 DT 15-JUN-2002 (Rel. 41, Created)
 DT 15-JUN-2002 (Rel. 41, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Tumor necrosis factor receptor superfamily member 13B (Transmembrane
 DE activator and CAML interactor).
 GN TNFRSF13B OR TACI.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE-Spleen;
 RX MEDLINE-21177254; PubMed-10881172;
 RA Yan M., Marsters S.A., Grewal I.S., Wang H., Ashkenazi A.,
 RA Dixit V.M.;
 *Identification of a receptor for Blys demonstrates a crucial role in
 *humoral immunity.";
 RL Nat. Immunol. 1:37-41(2000).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN-C57BL/6J; TISSUE-Lung;
 RX MEDLINE-21085660; PubMed-11217851;
 RA Kawai J., Shingawa A., Shibata K., Yoshino M., Itch M., Ishii Y.,
 RA Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
 RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamahata I.,
 RA Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
 RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
 RA Fleischmann W., Gaasterland T., Gissi C., King B., Kochwa H.,
 RA Kuehl P., Lewis S., Matsuo Y., Nikaide R., Tomita M., Wagner L., Washio T.,
 RA Schiml L.M., Straubli P., Suzuki R., Tomita M., Wagner L., Washio T.,
 RA Sakai K., Okido T., Furuno M., Kono H., Balderelli R., Barsh G.,
 RA Blake J., Botfield D., Bojunga N., Carninci P., de Bonaldo M.F.,
 RA Brownstein M.J., Bolt C., Fletcher C., Fujita M., Gariboldi M.,
 RA Gustingich S., Hill D., Hofmann M., Hume D.A., Kamuya M., Lee N.H.,
 RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombereis P.,
 RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
 RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
 RA Suzuki H., Toyooka K., Wang K.H., Weitz C., Whitaker C., Wilming L.,
 RA Wyszynski-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohsaki S.,

RA Hayashizaki Y.;
 RT "Functional annotation of a full-length mouse cDNA collection.";
 RL Nature 409:685-690(2001).
 RN [3]
 RP FUNCTION.
 RX MEDLINE-20341628; PubMed-10880535;
 RA Xia X.-Z., Treanor J., Senaldi G., Khare S.D., Boone T., Kelley M.,
 RA Theill L.E., Colombero A., Solovay I., Lee F., McCabe S., Elliott R.,
 RA Miner K., Hawkins N., Guo J., Stollin M., Yu G., Wang J., Delaney J.,
 RA Meng S.-Y., Boyle W.J., Hsu H.;
 RT "TACI is a TRAF-interacting receptor for TALL-1, a tumor necrosis
 RT factor family member involved in B cell regulation.";
 RL J. Exp. Med. 192:137-143(2000).
 RN [4]
 RP FUNCTION.
 RX MEDLINE-21322748; PubMed-11429548;
 RA Wang H., Marsters S.A., Baker T., Chan B., Lee W.P., Fu L., Tumas D.,
 RA Yan M., Dixit V.M., Ashkenazi A., Grewal I.S.;
 RT "TACI-1 ligand interactions are required for T cell activation and
 RT collagen-induced arthritis in mice.";
 RL Nat. Immunol. 2:632-637(2001).
 CC -1- FUNCTION: Receptor for TNFRSF13B/TACI/BAFF/Blys
 CC that binds both ligands with similar high affinity. Mediates
 CC calcineurin-dependent activation of NF-AT, as well as activation
 CC of NF-kappa-B and AP-1. Involved in the stimulation of B- and T-
 CC cell function and the regulation of humoral immunity (By
 CC similarity).
 CC -1- SUBUNIT: Binds TRAF2, TRAF5 and TRAF6. Binds the NH2-terminal
 CC domain of CAML with its C-terminus (By similarity).
 CC -1- SUBCELLULAR LOCATION: Type III membrane protein (Probable).
 CC -1- SIMILARITY: CONTAINS 2 TNFR-CYS REPEATS.
 CC
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 CC -----
 CC EMBL: AF257673; AAC00081.1; -
 CC EMBL: AK004668; BAB23457.1; -
 CC MGD: MGI:1889411; Tnftrsf13b.
 DR PROSITE: PS00652; TNFR-NGFR.1; 1.
 DR PROSITE: PS00652; TNFR-NGFR.2; 2.
 KW Receptor; Immune response; Signal-anchor; Transmembrane; Repeat.
 FT DOMAIN 1 128
 FT TRANSMEM 129 149
 FT
 FT DOMAIN 150 249
 FT REPEAT 5 38
 FT REPEAT 42 76
 FT DISULFID 6 19
 FT DISULFID 22 34
 FT DISULFID 26 38
 FT DISULFID 43 58
 FT DISULFID 61 72
 FT DISULFID 65 76
 FT CONFLICT 137 137
 FT SEQUENCE 249 AA; 26947 MW; CB2F2D61C2931D81 CRC64;
 SO
 Query Match 29.9%; Score 71.5; DB 1; Length 249;
 Best Local Similarity 35.3%; Pred. No. 0.055;
 Matches 12; Conservative 8; Mismatches 13; Indels 1; Gaps 1;
 QY 5 CSONEYFDSLHACIPQLNCSSNTPPLTCORC 38
 DB 6 CPRDQWDSRRKSCVSCALTCORS-ORTCDRC 38
 RESULT 4
 PKR5_MOUSE STANDARD; PRT; 1877 AA.
 ID PKR5_MOUSE

AC Q04592; Q62040; DT 01-FEB-1995 (Rel. 31, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Proprotein convertase subtilisin/kexin type 5 precursor (EC 3.4.21.-)
DE (Proteinase convertase PCS5) (Subtilisin/kexin-like protease PCS)
DE (Convertase PCS) (PC6) (Subtilisin-like proprotein convertase 6)
DE (SPC6).
GN PCS5.
OS Mus musculus (mouse).
OC Eukaryote; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE OF 330-1877 FROM N.A. (ISOFORM PCSB).
RC STRAIN=ICR; TISSUE=Intestine;
RX MEDLINE=93327934; PubMed=8335106;
RA Nakagawa T., Murakami K., Nakayama K.;
RT "Identification of an isoform with an extremely large Cys-rich region
of PC6, a Kex2-like processing endoprotease.";
RL FEBS Lett. 327:165-171(1993).
RL [2]
RN [3]
RP SEQUENCE FROM N.A. (ISOFORM PCSA).
RC TISSUE=Brain, and Intestine;
RX MEDLINE=93224489; PubMed=8468318;
RA Nakagawa T., Hosaka M., Torii S., Watanabe T., Murakami K.,
RA Nakayama K.;
RT "Identification and functional expression of a new member of the
mammalian Kex2-like processing endoprotease family: Its striking
structural similarity to PC6A.";
RL J. Biochem. 113:132-135(1993).
RN [4]
RP SEQUENCE FROM N.A. (ISOFORM PCSA).
RC TISSUE=Adrenal cortex;
RX MEDLINE=93342056; PubMed=8341687;
RA Lussion J., Vleau D., Hamelin J., Day R., Chretien M., Seldin N.G.;
RT "CDNA structure of the mouse and rat subtilisin/kexin-like PC5: a
candidate proprotein convertase expressed in endocrine and
nonendocrine cells.";
RL Proc. Natl. Acad. Sci. U.S.A. 90:6691-6695(1993).
RN [5]
RP PARTIAL SEQUENCE, AND SUBCELLULAR LOCATION.
RX MEDLINE=97103178; PubMed=8947550;
RA De Bie I., Marinkiewicz M., Malide D., Lazure C., Nakayama K.,
RA Bendayem M., Seldin N.G.;
RT "The isoforms of proprotein convertase PC5 are sorted to different
subcellular compartments.";
RL J. Cell Biol. 135:1261-1275(1996).
RN [5]
RP DEVELOPMENTAL EXPRESSION.
RX MEDLINE=96293359; PubMed=8698813;
RA Constam D.B., Calton M., Robertson E.J.;
RT "SPC4, SPC6, and the novel protease SPC7 are coexpressed with bone
morphogenetic proteins at distinct sites during embryogenesis.";
RL J. Cell Biol. 134:181-191(1996).
RN [6]
RP DEVELOPMENTAL EXPRESSION.
RX MEDLINE=97436919; PubMed=9291583;
RA Rancourt S.L., Rancourt D.E.;
RT "Murine subtilisin-like proteinase SPC6 is expressed during embryonic
implantation, somitogenesis, and skeletal formation.";
RL Dev. Genet. 21:75-81(1997).
RN [7]
RP FUNCTION: LIKELY TO REPRESENT A WIDESPREAD ENDOPTASE ACTIVITY
WITHIN THE CONSTITUTIVE AND REGULATED SECRETORY PATHWAY. CAPABLE
OF CLEAVAGE AT THE RX(K/R)R CONSENSUS MOTIF. MAY BE RESPONSIBLE
FOR THE MATURATION OF GASTROINTESTINAL PEPTIDES. MAY BE INVOLVED
IN THE CELLULAR PROLIFERATION OF ADRENAL CORTEX VIA THE ACTIVATION
OF GROWTH FACTORS.
RN [8]
RP CATALYTIC ACTIVITY: RELEASE OF MATURE PROTEINS FROM THEIR
PROPEPTIC BY CLEAVAGE OF ARG-XAA-YAA-ARG-|-ZAA BONDS, WHERE XAA
CAN BE ANY AMINO ACID AND YAA IS ARG OR LYS.
RN [9]
RP SUBCELLULAR LOCATION: PCSA IS SECRETED THROUGH THE REGULATED
SECRETORY PATHWAY. PCSB IS A TYPE I MEMBRANE PROTEIN LOCALIZED TO

CC	A PARACELLULAR POST-GOLGI NETWORK COMPARTMENT IN COMMUNICATION WITH EARLY ENDOSOMES.
CC	-1- ALTERNATIVE PRODUCTS: AT LEAST 2 ISOFORMS: PCSB/LONG (SHOWN HERE)
CC	AND PCSA/SHORT: ARE PRODUCED BY ALTERNATIVE SPLICING.
CC	-1- TISSUE SPECIFICITY: PCSA IS EXPRESSED IN MOST TISSUES BUT IS MOST ABUNDANT IN THE INTESTINE AND ADRENALS. PCSB IS EXPRESSED IN THE INTESTINE, ADRENALS AND LUNG BUT NOT IN THE BRAIN.
CC	-1- DEVELOPMENTAL STAGE: WEAKLY EXPRESSED THROUGHOUT THE EMBRYO, EXCEPT IN THE DEVELOPING NERVOUS SYSTEM, THE KIDNEY AND THE LIVER, BUT MARKEDLY UPREGULATED AT DISCRETE SITES DURING DEVELOPMENT. AT E6.5, PROMINENT EXPRESSION OBSERVED IN DIFFERENTIATED DECIDUA. AT E7.5, INTENSE EXPRESSION IN EXTRAEMBRYONIC ENDODERM, AMNION AND NASCENT MESODERM. AT 8.5, ABUNDANT EXPRESSION IN SOMITES AND YOLK SAC, FOLLOWED BY A CONFINATION TO DERMATOTOME COMPARTMENT. BETWEEN E9.5 AND E11.5, ABUNDANT EXPRESSION IN AER (THICKENED ECTODERMAL CELLS OF LIMB BUDS). AT E12.5, EXPRESSION IN THE LIMBS IS CONFINED TO THE CONDENSING MESENCHYM SURROUNDING THE CARTILAGE. AT THIS STAGE, STRONG EXPRESSION ALSO DETECTED IN VERTEBRAL AND FACIAL CARTILAGE PRIMORDIA AND IN THE MUSCLE OF THE TONGUE. AT E16.5, ABUNDANT EXPRESSION IN EPITHELIAL CELLS OF THE INTESTINAL VILLI.
CC	ISOFORM A IS MOST ABUNDANT AT ALL STAGES BUT SIGNIFICANT LEVELS OF ISOFORM B OCCUR AT E12.5.
CC	-1- DOMAIN: THE PROPEPTIDE DOMAIN ACTS AS AN INTRAMOLECULAR CHAPERONE ASSISTING THE FOLDING OF THE ZYMOGEN WITHIN THE ENDOPLASMIC RETICULUM.
CC	-1- DOMAIN: AC 1 AND AC 2 (CLUSTERS OF ACIDIC AMINO ACIDS) CONTAIN SORTING INFORMATION. AC 1 DIRECTS TGN LOCALIZATION AND INTERACTS WITH THE TGN SORTING PROTEIN PACS-1.
CC	-1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S8.
CC	-1- SIMILARITY: CONTRAINS 1 HOMO B/P DOMAIN.
CC	-----
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CC	-----
DR	EMBL; D17583; BAA04507.1; -
DR	EMBL; D12619; BAA02143.1; -
DR	EMBL; L14932; AAA74636.1; -
DR	PIR; JX0248; JX0248.
DR	PIR; A48225; A48225.
DR	HSSP; O99405; IMPF.
DR	MEROPS; S08_076; -
DR	MED; MGI:97515; PCSK5.
DR	InterPro: IPR000361; EGF-like.
DR	InterPro: IPR002174; Furin-like.
DR	InterPro: IPR002884; P_domain.
DR	InterPro: IPR000209; Peptidase-S8.
DR	Pfam: PF00082; Peptidase_S8; 1.
DR	Pfam: pf01483; P; PARTIAL.
DR	PRINTS; PR00723; SUBTILISIN.
DR	PRODOM; PD000717; P_domain; 1.
DR	SMART; SM00181; EGF; 3.
DR	SMART; SM00001; EGF_Like; 2.
DR	SMART; SM00261; FU; 22.
DR	PROSITE; PS00136; SUBTILASE_ASP; 1.
DR	PROSITE; PS00137; SUBTILASE_HIS; 1.
DR	PROSITE; PS00138; SUBTILASE_SER; 1.
KW	Hydrolase; Serine protease; Glycoprotein; zymogen; signal;
KW	Cleavage on pair of basic residues; Repeat; Alternative splicing;
KM	Transmembrane.
FT	SIGNAL 1 34
FT	PROPEP 35 116
FT	CHAIN 117 1877
FT	-----
FT	DOMAIN 117 1768
FT	TNSMEM 1769 1789
FT	DOMAIN 1790 1877
FT	DOMAIN 117 452
FT	DOMAIN 464 602
FT	-----
FT	DOMAIN 464 602
FT	HOMO B.
FT	-----
FT	PROTEIN CONVERTASE SUBTILISIN/KEXIN TYPE 5.
FT	EXTRACELLULAR (POTENTIAL).
FT	POTENTIAL.
FT	CYTOSOLASMIC (POTENTIAL).
FT	CATALYTIC.
FT	HOMO B.

FT DOMAIN 638 1753 CYS-RICH MOTIF (CRM) REGION.
 FT DOMAIN 1825 1844 AC 1.
 FT DOMAIN 1856 1877 AC 2.
 FT SITE 116 117 CLEAVAGE (AUTO-) (BY SIMILARITY).
 FT SITE 521 523 CELL ATTACHMENT SITE (POTENTIAL).
 FT ACT_SITE 173 173 CHARGE RELAY SYSTEM (BY SIMILARITY).
 FT ACT_SITE 214 214 CHARGE RELAY SYSTEM (BY SIMILARITY).
 FT ACT_SITE 388 388 CHARGE RELAY SYSTEM (BY SIMILARITY).
 FT CARBOHYD 227 227 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 383 383 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 667 667 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 754 754 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 804 804 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 854 854 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 951 951 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 1016 1016 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 1220 1220 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 1317 1317 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 1523 1523 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 1711 1711 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 1733 1733 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT VARSPIC 878 915 ATESWAGGFCMLYKKNKLNQKRYLQQLCKCTFPG
 (IN ISOPFORM PC5A).
 FT VARSPIC 916 1877 MISSING (IN ISOPFORM PC5A).
 FT SEQUENCE 1877 AA: 209287 MW: EC850E2DF20EA1C3 CRC64:
 SO
 Query Match 29.1%; Score 69.5; DB 1; Length 1877;
 Best Local Similarity 36.8%; Pred. No. 0.61;
 Matches 14; Conservative 5; Mismatches 14; Indels 5; Gaps 1;
 QY 4 QCSQNEFYDLSLHACIPGQRCSSNPP-----LTCOR 36
 DB 1480 ECANVEYWDGSHRCPCPKKRCSCGSPEDOCYTPR 1517
 RESULT 5
 ZAN_MOUSE STANDARD: PRT: 5376 AA.
 ID ZAN_MOUSE
 AC 088799: 008647:
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Zonadhesin precursor.
 GN ZAN.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE-Testis;
 RX MEDLINE=98123114; PubMed=9452463;
 RA Gao Z., Garbers D.L.;
 RT *Species diversity in the structure of zonadhesin, a sperm-specific
 RT membrane protein containing multiple cell adhesion molecule-like
 RT domains.*;
 RL J. Biol. Chem. 273:3415-3421(1998).
 RN [2]
 RP SEQUENCE OF 4864-5376 FROM N.A.
 RC TISSUE-Testis;
 RX MEDLINE=97271566; PubMed=9126492;
 RA Gao Z., Haruni T., Garbers D.L.;
 RT *Chromosome localization of the mouse zonadhesin gene and the human
 RT zonadhesin gene (ZAN).*;
 RL Genomics 41:119-122(1997).
 CC -1- FUNCTION: BINDS IN A SPECIES-SPECIFIC MANNER TO THE ZONA PELLUCIDA
 CC SIGNALING.
 CC -1- SUBUNIT: PROBABLY FORMS COVALENT OLIGOMERS.
 CC -1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN, EXCLUSIVELY ON THE
 CC APICAL REGION OF THE SPERM HEAD.
 CC -1- TISSUE SPECIFICITY: IN TESTIS; PRIMARILY IN HARPOID SPERMATIDS.

CC -1- DOMAIN: THE MAM DOMAINS PROBABLY MEDIATES SPERM ADHESION TO THE
 CC ZONA PELLUCIDA.
 CC -1- DOMAIN: DURING SPERM MIGRATION THROUGH THE REPRODUCTIVE TRACTS,
 CC THE MUCIN-LIKE DOMAIN MIGHT INHIBIT INAPPROPRIATE TRAPPING OF
 CC SPERMATOZOIA OR PROMOTING ADHESION TO THE CVIDUCTAL ISTHMUS.
 CC -1- DOMAIN: THE WMD DOMAIN 2 MAY MEDIATE COVALENT
 CC OLIGOMERIZATION (BY SIMILARITY TO HUMAN INTESTINL MUCIN MUC2).
 CC -1- SIMILARITY: CONTAINS 3 MAM DOMAINS.
 CC -1- SIMILARITY: CONTAINS 25 WMD DOMAINS.
 CC -1- SIMILARITY: CONTAINS 1 EGF-LIKE DOMAIN.
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 CC or send an email to license@isb-sib.ch).
 CC
 CC EMBL: U97068; AAC26680.1; -;
 CC EMBL: U83190; AAC53125.1; -;
 CC MGD: MGI:106656; zan.
 CC InterPro: IPR000561; EGF-like.
 CC InterPro: IPR003645; FN1.
 CC InterPro: IPR000998; MAM_domain.
 CC InterPro: IPR002919; T1L_CysRich.
 CC InterPro: IPR003328; T1L_CysRich.
 CC InterPro: IPR001007; VWF_C.
 CC InterPro: IPR01846; VWF_D.
 CC Pfam: PF00094; vwd; 4.
 CC Pfam: PF00629; MAM; 3.
 CC Pfam: PF01826; T1L; 25.
 CC Pfam: PF02345; T1L; 25.
 CC SMART: SM00181; EGF; 2.
 CC SMART: SM00274; FN1; 11.
 CC SMART: SM00137; MAM; 2.
 CC SMART: SM00214; VMC; 17.
 CC SMART: SM00216; VMD; 4.
 CC PROSITE: PS00023; EGF_1; 1.
 CC PROSITE: PS01186; EGF_2; 18.
 CC PROSITE: PS00740; MAM_1; FALSE_NEG.
 CC PROSITE: PS0060; MAM_2; 3.
 CC Signal: Glycoprotein; Transmembrane; EGF-like domain; Cell adhesion;
 CC Repeat.
 CC KW SIGNAL.
 CC FT CHAIN 1 17
 CC FT DOMAIN 18 5376
 CC FT TRANSMEM 5311 5337
 CC FT DOMAIN 5338 5376
 CC FT DOMAIN 45 210
 CC FT DOMAIN 215 374
 CC FT DOMAIN 377 542
 CC FT DOMAIN 547 1170
 CC FT DOMAIN 1171 1280
 CC FT DOMAIN 1281 1659
 CC FT DOMAIN 1670 2056
 CC FT DOMAIN 2057 2459
 CC FT DOMAIN 2460 2579
 CC FT DOMAIN 2580 2699
 CC FT DOMAIN 2700 2819
 CC FT DOMAIN 2820 2939
 CC FT DOMAIN 2940 3059
 CC FT DOMAIN 3060 3179
 CC FT DOMAIN 3180 3299
 CC FT DOMAIN 3300 3416
 CC FT DOMAIN 3417 3536
 CC FT DOMAIN 3537 3656
 CC FT DOMAIN 3657 3776
 CC FT DOMAIN 3777 3892
 CC FT DOMAIN 3893 4029
 CC FT DOMAIN 4029 4148
 CC FT DOMAIN 4149 4263
 CC
 CC POTENTIAL.
 CC ZONADHESIN.
 CC EXTRACELLULAR (POTENTIAL).
 CC POTENTIAL.
 CC CYTOPLASMIC (POTENTIAL).
 CC MAM 1.
 CC MAM 2.
 CC 80 X HEPTAPEPTIDE REPEATS (APPROXIMATE)
 CC (MUCIN-LIKE DOMAIN).
 CC WMD 1 (PARTIAL).
 CC WMD 2.
 CC WMD 3.
 CC WMD 4.
 CC WMD 5 (PARTIAL).
 CC WMD 6 (PARTIAL).
 CC WMD 7 (PARTIAL).
 CC WMD 8 (PARTIAL).
 CC WMD 9 (PARTIAL).
 CC WMD 10 (PARTIAL).
 CC WMD 11 (PARTIAL).
 CC WMD 12 (PARTIAL).
 CC WMD 13 (PARTIAL).
 CC WMD 14 (PARTIAL).
 CC WMD 15 (PARTIAL).
 CC WMD 16 (PARTIAL).
 CC WMD 17 (PARTIAL).
 CC WMD 18 (PARTIAL).
 CC WMD 19 (PARTIAL).

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FT DOMAIN 4264 4283 WMD 20 (PARTIAL).
FT DOMAIN 4384 4503 WMD 21 (PARTIAL).
FT DOMAIN 4504 4623 WMD 22 (PARTIAL).
FT DOMAIN 4624 4743 WMD 23 (PARTIAL).
FT DOMAIN 4744 4863 WMD 24 (PARTIAL).
FT DOMAIN 4864 5261 WMD 25.
FT DOMAIN 5262 5274 EGF-LIKE.
FT DISULFID 5263 5283 BY SIMILARITY.
FT DISULFID 5285 5294 BY SIMILARITY.
FT CARBOHYD 339 339 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 499 499 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 1216 1216 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 1239 1239 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 1314 1314 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 1814 1814 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 1908 1908 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 1933 1933 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 2028 2028 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 2111 2111 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 2142 2142 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 2332 2332 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 2533 2533 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 2575 2575 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 2692 2692 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 2812 2812 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 3052 3052 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 3065 3065 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 3144 3144 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 3172 3172 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 3288 3288 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 3292 3292 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 3782 3782 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 4005 4005 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 4136 4136 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 4243 4243 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 4254 4254 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 4335 4335 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 4376 4376 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 4586 4586 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 5136 5136 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 5252 5252 N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ SEQUENCE 5376 AA: 579908 MW: 0E44DB77DF2A2620 CRC64:

Query Match 29.18: Score 69.5; DB 1: Length 5376;
Best Local Similarity 36.88; Pred. No. 1.6;
Matches 14: Conservative 5; Mismatches 16; Indels 3; Gaps 2;

OY 4 QCSQNFPSDLHACIP-CQLRCSSNTP-PLTCQRYC 38
Db 3299 QCPNSQFTDCLPSCVPCSNRCVETSPVSSCRECC 3336

RESULT 5
T13X_HUMAN STANDARD; PRT; 293 AA.
AC O14836;
DT 15-JUN-2002 (Rel. 41, Created)
DT 15-JUN-2002 (Rel. 41, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Tumor necrosis factor receptor superfamily member 13B (Transmembrane
DE activator and CAML interactor).
GN TNFRSF13B OR TACI.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=B-cell;
RX MEDLINE=97458245; PubMed=9311921;
RA von Buelow G., U., Bram R.J.;
RA "NF-AT activation induced by a CAML-interacting member of the tumor

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RT necrosis factor receptor superfamily.";
RL Science 278:138-141(1997).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Blood;
RA Strausberg R.;
RL Submitted (Apr-2002) to the EMBL/GenBank/DBJ databases.
RN [3]
RX MEDLINE=20519647; PubMed=10956646;
RA Wu Y., Bressette D., Carrell J.A., Kaufman T., Feng P., Taylor K.,
RA Can Y., Cho Y.H., Garcia A.D., Gollatz E., Dimke D., Lafleur D.,
RA Mlyone T.S., Nardelli B., Wel P., Ruben S.M., Ullrich S.J.,
RT Olsen H.S., Kanakiraj P., Moore P.A., Baker K.P.;
RT "Tumor necrosis factor (TNF) receptor superfamily member TACI is a
RL high affinity receptor for TNF family members APRIL and BLys.";
RN J. Biol. Chem. 275:35478-35485(2000).
RN [4]
RX MEDLINE=21170294; PubMed=10973284;
RA Yu G., Boone T., Delaney J., Hawkins N., Kelley M., Ramakrishnan M.,
RA McCabe S., Qiu W.R., Kornuc M., Xia X.-Z., Guo J., Stolina M.,
RA Boyle W.J., Sarosi I., Hsu H., Senaldi G., Thell L.E.;
RT APRIL and TACI-1 and receptors BCMA and TACI: system for regulating
RN humoral immunity.";
RL Nat. Immunol. 1:252-256(2000).
CC - FUNCTION: Receptor for TNFRSF13B/TACI1/BAFF/BLYS
CC that binds both ligands with similar high affinity. Mediates
CC calcineurin-dependent activation of NF-AT, as well as activation
CC of NF-kappa-B and AP-1. Involved in the stimulation of B- and T-
CC cell function and the regulation of humoral immunity.
CC - SUBUNIT: Binds TRAF2, TRAF5 and TRAF6. Binds the NH2-terminal
CC domain of CAML with its C-terminus.
CC - TISSUE SPECIFICITY: Highly expressed in spleen, thymus, small
CC intestine and peripheral blood leukocytes. Expressed in resting B-
CC cells and activated T-cells, but not in resting T-cells.
CC - SIMILARITY: CONTAINS 2 TNFR-CYS REPEATS.
CC - CAUTION: It is uncertain whether Met-1 or Met-31 is the initiator.
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CC -----
DR EMBL: AF023614; AAC51790.1; -
DR EMBL: BC028072; AAH28072.1; -
DR Gene: HGNC:18153; TNFRSF13B.
DR MIM: 604907; -
DR InterPro: IPR001368; TNFR-C6.
DR PROSITE: PS00652; TNFR_NGFR_1; 1.
DR PROSITE: PS50050; TNFR_NGFR_2; FALSE_NEG.
KW Receptor; Immune response; Signal anchor; Transmembrane; Glycoprotein;
KW Repeat.
FT DOMAIN 1 165 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 166 186 SIGNAL-ANCHOR (TYPE III MEMBRANE PROTEIN)
FT REPEAT 33 67 CYTOPLASMIC (POTENTIAL).
FT REPEAT 70 104 TNFR-CYS 1.
FT DISULFID 34 47 TNFR-CYS 2.
FT DISULFID 47 62 BY SIMILARITY.
FT DISULFID 50 62 BY SIMILARITY.
FT DISULFID 54 66 BY SIMILARITY.
FT DISULFID 71 86 BY SIMILARITY.
FT DISULFID 89 100 BY SIMILARITY.
FT DISULFID 93 104 BY SIMILARITY.
FT CARBOHYD 128 128 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CONFLICT 251 251 P -> L (IN REF. 2).
SQ SEQUENCE 293 AA: 31816 MW: 411799F3DE17A5EB CRC64:

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Query Match: 28.2% Score 67.5; DB 1; Length 293;
Best Local Similarity 30.6%; Pred. No. 0.2;
Matches 11; Conservative 9; Mismatches 15; Indels 1; Gaps 1

5 CSONEYFDSILHACIPQJRCSSNTPPLTCORYCNA 40
1 : 11 11 1 : 1 : 11 :
Db 34 CPEQYWDPLIGTCMCKTICNHOS -ORTCAFCRS 68

RESULT 7
T13C_MOUSE
ID T13C_MOUSE STANDARD: PRT: 175 AA.
AC QSD8D0;
DT 15-JUN-2002 (Rel. 41, Created)
DT 15-JUN-2002 (Rel. 41, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Tumor necrosis factor receptor superfamily member 13C (B cell-
activating factor receptor) (BAFF receptor) (BAFF-R) (Blys receptor
3) (B-cell maturation defect)
DEF TMRSP13C OR BAFFR OR BCMD OR BR3.
OS Mus musculus (mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sclirognathi; Muridae; Mus.
OX NCBI_TaxId=10090;
RN [1]
RP SEQUENCE FROM N.A. (ISOFORMS 1 AND 2).
RC STRAIN-BALB/C; TISSUE-B-cell lymphoma;
RX MEDLINE-21442025; PubMed-11509592;
RA Thompson J.S., Bixler S.A., Qian F., Vora K., Scott M.L.,
Caechoen T.G., Hession C., Schneider P., Sling I.D., Mullen C.,
Strauch K., Zafari M., Benjamin C.D., Tschopp J., Browning J.L.,
Ambrose C.;
RT "BAFF-R, a newly identified TNF receptor that specifically interacts
with BAFF.";
RL Science 293:2108-2111(2001).
RN [2]
RP SEQUENCE FROM N.A. (ISOFORM 1), AND DISEASE.
RC STRAIN-A/J;
RX MEDLINE-21475520; PubMed-11591325;
RA Yan M., Brady J.R., Chan B., Lee W.P., Hsu B., Harless S.M.,
Cancro M.P., Grewal I.S., Dixit V.M.;
RT "Identification of a novel receptor for B lymphocyte stimulator that
is mutated in a mouse strain with severe B cell deficiency.";
RL Curr. Biol. 11:1547-1552(2001).
RN [3]
RP SEQUENCE FROM N.A. (ISOFORM 1).
RC STRAIN-C57BL/6J; TISSUE-Small intestine;
RX MEDLINE-21085660; PubMed-11217851;
RA Kawai T., Shingawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
Aikawa T., Hara A., Fukunishi Y., Kono H., Adachi T., Fukuda S.,
Alzawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamataka I.,
Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
Fleischmann W., Gaasterland T., Gissi G., King B., Kochwa H.,
Knehl P., Lewis S., Matsuo Y., Nikolaic I., Pesole G., Quackenbush J.,
Schirral L.M., Stadl F., Suzuki R., Tomita M., Wagner L., Washio T.,
Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
Borenstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
Gastlisch S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
Lyons P., Marchionni L., Mashima J., Mazzarelli J., Monbaets P.,
Nordone P., Ring B., Ringwald M., Rodriguez T., Sakamoto N.,
Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
Suzuki H., Toyooka K., Wang K.H., Weitz C., Whitaker C., Wilming L.,
Wyszynski B., Yoshida K., Hasegawa Y., Kawaji H., Kohsaki S.,
Hayashizaki Y.;
RT "Functional annotation of a full-length mouse cDNA collection.";
RL Nature 409:685-690(2001).
RN [4]
RP MEDLINE-21614654; PubMed-11747827;
RX Harless S.M., Lentz V.M., Seh A.P., Hsu B.L., Clise-Dwyer K.,
Hilbert D.M., Hayes C.E., Cancro M.P.;

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RT  "Competition for BLVS-mediated signaling through Bcnd/BK3 regulates
RL  peripheral B lymphocyte numbers."
CC  Curr. Biol. 11:1986-1989(2001).
CC  -1- FUNCTION: B-cell receptor specific for TNFSF13B/TALL1/BAPF/BLVS.
CC  Promotes the survival of mature B-cells and the B-cell response.
CC  -1- SUBCELLULAR LOCATION: Type III membrane protein (Probable).
CC  -1- ALTERNATIVE PRODUCTS: 2 isoforms: 1 (shown here) and 2; are
CC  produced by alternative splicing.
CC  -1- TISSUE SPECIFICITY: Highly expressed in spleen and testis;
CC  detected at lower levels in lung and thymus.
CC  -1- DISEASE: Defects in TNFSF13C cause of severe B-cell
CC  deficiency. B-cell deficient strain A/WySnJ has a 4.7 kb insertion
CC  in the BAPF gene leading to an altered C-terminus. The mutant RNA
CC  is not detectable. B-cell lymphoproliferosis is normal, but the life
CC  span of peripheral B-cells is much reduced.
CC  -1- SIMILARITY: CONTAINS 1 TNFR-CYS REPEAT.
CC  -----
CC  "This SWISS-PROT entry is copyright. It is produced through a collaboration
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CC  use by non-profit institutions as long as its content is in no way
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CC  or send an email to license@isb-sib.ch).
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conserved in humans and chickens".
 CC Arterioscler. Thromb. Vasc. Biol. 17:996-1002(1997).
 CC -1- FUNCTION: LIKELY TO BE A MULTIFUNCTIONAL ENDOCYTIC RECEPTOR, THAT
 CC MAY BE IMPLICATED IN THE UPTAKE OF LIPOPROTEINS AND OF PROTEASES.
 CC BINDS LDL, THE MAJOR CHOLESTEROL-CARRYING LIPOPROTEIN OF PLASMA,
 CC AND TRANSPORTS IT INTO CELLS BY ENDOCYTOSIS. BINDS THE RECEPTOR-
 CC ASSOCIATED PROTEIN (RAP). COULD PLAY A ROLE IN CELL-CELL
 CC INTERACTION. BOTH ESTROGEN STATUS AND CHOLESTEROL LEVELS LACK
 CC REGULATORY EFFECTS ON THIS RECEPTOR.
 CC -1- SUBCELLULAR LOCATION: Type I membrane protein (Potential).
 CC -1- TISSUE SPECIFICITY: EXPRESSED ABUNDANTLY IN BRAIN. PRESENT IN THE
 CC TESTES, ADRENAL GLANDS AND DETECTABLE IN THE LUNG.
 CC -1- SIMILARITY: CONTAINS 5 BNR REPEATS.
 CC -1- SIMILARITY: CONTAINS 1 EGF-LIKE DOMAIN.
 CC -1- SIMILARITY: CONTAINS 11 LDL-RECEPTOR CLASS A DOMAINS.
 CC -1- SIMILARITY: CONTAINS 2 FIBRONECTIN TYPE III-LIKE DOMAINS.
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 CC -----
 DR EMBL: Y08109; CAA69324.1; -
 DR HSSP: P01130; 1A1J.
 DR InterPro: IPR000561; EGF-like.
 DR InterPro: IPR003961; FN_III.
 DR InterPro: IPR002860; GH_BNR.
 DR InterPro: IPR002172; LDL_receptor_A.
 DR InterPro: IPR000033; Ldl_receptor_rep.
 DR Pfam: PF00057; fnc_1.
 DR Pfam: PF00057; Ldl_recept_a; 11.
 DR Pfam: PF00056; Ldl_recept_b; 5.
 DR Pfam: PF00202; BNR_5.
 DR PRINTS: PR00261; LDLRECEPTOR.
 DR SMART: SM00181; EGF; 1.
 DR SMART: SM00060; FN3; 1.
 DR SMART: SM00192; LDLa; 11.
 DR SMART: SM00135; LV; 5.
 DR PROSITE: PS01166; EGF_2; 1.
 DR PROSITE: PS01209; LDLRA_1; 11.
 DR PROSITE: PS50066; LDLRA_2; 11.
 DR Endocytosis: Receptor; EGF-like domain; Repeat; Glycoprotein; LDL;
 KM Lipid transport; Cholesterol metabolism.
 FT NON_TER 1
 FT REPEAT 43 54 BNR 1.
 FT REPEAT 139 150 BNR 2.
 FT REPEAT 348 359 BNR 3.
 FT REPEAT 428 439 BNR 4.
 FT REPEAT 469 480 BNR 5.
 FT DOMAIN 710 884 5 X APPROXIMATE YWTD REPEATS.
 FT REPEAT 710 713 1.
 FT REPEAT 754 757 2.
 FT REPEAT 798 801 3.
 FT REPEAT 841 844 4.
 FT REPEAT 881 884 5.
 FT REPEAT 933 979 EGF-LIKE.
 FT DOMAIN 983 1021 LDL-RECEPTOR CLASS A 1.
 FT DOMAIN 1022 1062 LDL-RECEPTOR CLASS A 2.
 FT DOMAIN 1063 1100 LDL-RECEPTOR CLASS A 3.
 FT DOMAIN 1103 1143 LDL-RECEPTOR CLASS A 4.
 FT DOMAIN 1143 1180 LDL-RECEPTOR CLASS A 5.
 FT DOMAIN 1180 1224 LDL-RECEPTOR CLASS A 6.
 FT DOMAIN 1230 1268 LDL-RECEPTOR CLASS A 7.
 FT DOMAIN 1273 1312 LDL-RECEPTOR CLASS A 8.
 FT DOMAIN 1324 1362 LDL-RECEPTOR CLASS A 9.
 FT DOMAIN 1376 1415 LDL-RECEPTOR CLASS A 10.
 FT DOMAIN 1419 1457 LDL-RECEPTOR CLASS A 11.
 FT DOMAIN 1462 1551 FIBRONECTIN TYPE-III 1.
 FT DOMAIN 1559 >1592 FIBRONECTIN TYPE-III 2.
 FT DISULFID 985 997 BY SIMILARITY.

FT DISULFID 992 1010 BY SIMILARITY.
 FT DISULFID 1004 1019 BY SIMILARITY.
 FT DISULFID 1024 1038 BY SIMILARITY.
 FT DISULFID 1032 1051 BY SIMILARITY.
 FT DISULFID 1043 1060 BY SIMILARITY.
 FT DISULFID 1065 1077 BY SIMILARITY.
 FT DISULFID 1072 1090 BY SIMILARITY.
 FT DISULFID 1084 1099 BY SIMILARITY.
 FT DISULFID 1105 1117 BY SIMILARITY.
 FT DISULFID 1112 1130 BY SIMILARITY.
 FT DISULFID 1124 1141 BY SIMILARITY.
 FT DISULFID 1145 1155 BY SIMILARITY.
 FT DISULFID 1150 1168 BY SIMILARITY.
 FT DISULFID 1162 1222 BY SIMILARITY.
 FT DISULFID 1232 1244 BY SIMILARITY.
 FT DISULFID 1239 1257 BY SIMILARITY.
 FT DISULFID 1251 1266 BY SIMILARITY.
 FT DISULFID 1275 1288 BY SIMILARITY.
 FT DISULFID 1283 1301 BY SIMILARITY.
 FT DISULFID 1295 1310 BY SIMILARITY.
 FT DISULFID 1333 1351 BY SIMILARITY.
 FT DISULFID 1345 1360 BY SIMILARITY.
 FT CARBOHYD 6 6 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 65 65 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 275 275 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 337 337 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 523 523 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 581 581 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 725 725 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 778 778 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 975 975 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 1098 1098 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 1152 1152 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 1366 1366 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 1454 1454 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 1514 1514 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT NON_TER 1592 1592 N-LINKED (GLCNAC. . .) (POTENTIAL).
 SQ SEQUENCE 1592 AA: 178409 MW: 24E0A55A231B203 CRC64:
 Query Match 25.9%; Score 62; DB 1; Length 1592;
 Best Local Similarity 33.3%; Pred. No. 4; 4;
 Matches 15; Conservative 6; Mismatches 18; Indels 6; Gaps 2;
 Oy 3 GGCSONEFDSLLACIP-----COLR--GSSNTPPLTCORYNAS 41
 Db 1376 GRCSTFEFCQHLKICIPMKRCGRRCODGDRSCPTSHSL 1420
 RESULT 9
 SSPO_BOVIN STANDARD; PRT: 867 AA.
 AC p98167;
 DI 01-OCT-1996 (Rel. 34, Created)
 DI 01-OCT-1996 (Rel. 34, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE SCO-spondin (Fragment).
 OS Bos taurus (Bovine).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
 OC Bovidae; Bovinae; Bos.
 ON NCBI_TaxID=9913;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Endomycyte;
 RX MEDLINE=96338614; PubMed=8743952;
 RA Gobron S., Monnerie H., Meinel A., Creveaux I., Lehmann W.,
 RA Lamelle D., Dastugue B., Meinel A.;
 RT "SCO-spondin: a new member of the thrombospondin family secreted by
 RT the subcommissural organ is a candidate in the modulation of neuronal
 RT aggregation.";
 RL J. Cell Sci. 109:1053-1061(1996).
 CC -1- FUNCTION: INVOLVED IN THE MODULATION OF NEURONAL AGGREGATION.
 CC -1- SUBCELLULAR LOCATION: Extracellular.

CC -1- TISSUE SPECIFICITY: SUBCOMMISSURAL ORGAN.
CC -1- DEVELOPMENTAL STAGE: EMBRYO.
CC -1- SIMILARITY: BELONGS TO THE THROMBOSPONDIN FAMILY.
CC -1- SIMILARITY: CONTAINS AT LEAST 4 TSP TYPE-1 DOMAINS.
CC -1- SIMILARITY: CONTAINS AT LEAST 2 EGF-LIKE DOMAINS.
CC -1- SIMILARITY: CONTAINS AT LEAST 1 F5/8 TYPE C DOMAIN.
CC -1- SIMILARITY: CONTAINS AT LEAST 3 LDL-RECEPTOR CLASS A DOMAINS.

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CC EMBL: X93922, CAA63815.1, -.
CC HSSP: P01130; IAUJ.
CC InterPro: IPR000421; FA58.C.
CC InterPro: IPR002172; LDL_receptl_A.
CC InterPro: IPR002919; TIL_Cysrich.
CC InterPro: IPR000884; TSP1.
CC InterPro: IPR001007; VWF.C.
CC Pfam: PF000057; LDL_receptl_a; 3.
CC Pfam: PF000090; tsp_1; 4.
CC Pfam: PF00093; vwc; 1.
CC Pfam: PF00754; F5_F8_Type-C; 1.
CC Pfam: PF01826; TIL; 1.
CC SMART: SM00231; FA58C; 1.
CC SMART: SM00192; LDLA; 3.
CC SMART: SM00209; TSP1; 4.
CC SMART: SM00214; VMC; 1.
CC PROSITE: PS01285; FA58C_1; 1.
CC PROSITE: PS01286; FA58C_2; 1.
CC PROSITE: PS01209; LDLRA_1; 3.
CC PROSITE: PS50068; LDLRA_2; 3.
CC PROSITE: PS50092; TSP1; 4.
CC Glycoprotein; Cell adhesion; Calcium-binding; Repeat; EGF-like domain.
KW NON_TER 1 1
FT DOMAIN 1 26 81 TSP TYPE-1 1.
FT DOMAIN 103 142 EGF-LIKE 1.
FT DOMAIN 143 180 EGF-LIKE 2.
FT DOMAIN 185 243 TSP TYPE-1 2.
FT DOMAIN 344 502 F5/8 TYPE C.
FT DOMAIN 506 544 LDL-RECEPTOR CLASS A 1.
FT DOMAIN 663 701 LDL-RECEPTOR CLASS A 2.
FT DOMAIN 723 761 LDL-RECEPTOR CLASS A 3.
FT DOMAIN 762 813 TSP TYPE-1 3.
FT DOMAIN 814 867 TSP TYPE-1 4.
FT DISULFD 107 122 BY SIMILARITY.
FT DISULFD 116 127 BY SIMILARITY.
FT DISULFD 129 141 BY SIMILARITY.
FT DISULFD 147 166 BY SIMILARITY.
FT DISULFD 149 169 BY SIMILARITY.
FT DISULFD 171 179 BY SIMILARITY.
FT DISULFD 344 502 BY SIMILARITY.
FT DISULFD 508 520 BY SIMILARITY.
FT DISULFD 515 533 BY SIMILARITY.
FT DISULFD 527 542 BY SIMILARITY.
FT DISULFD 665 677 BY SIMILARITY.
FT DISULFD 672 690 BY SIMILARITY.
FT DISULFD 684 699 BY SIMILARITY.
FT DISULFD 725 737 BY SIMILARITY.
FT DISULFD 732 750 BY SIMILARITY.
FT DISULFD 744 759 BY SIMILARITY.
FT CARBOHD 88 88 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHD 309 309 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CAROHD 409 409 N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ SEQUENCE 867 AA; 91817 MW; 9538F2108E787B49 CRC64;
Query Match 25.1%; Score 60; DB 1; Length 867;
Best Local Similarity 42.9%; Pred. NO. 4.4;

Matches 9; Conservative 3; Mismatches 9; Indels 0; Gaps 0;
Oy 14 ILMACIPCOLRCSSNTPPLTC 34
: |||:| | : 11
Db 96 VPRACVPCPLTCDDISQATC 116

RESULT 10
ID CLRL_MOUSE STANDARD; PRT; 3034 AA.
AC 035161;
DT 15-JUN-2002 (Rel. 41, Created)
DT 15-JUN-2002 (Rel. 41, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Cadherin EGF LAG seven-pass G-type receptor 1 precursor.
GN CELSR1
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX PubMed=9858697;
RA Hadjantonakis A.-K., Formstone C.J., Little P.F.R.,
RT McElstl is an evolutionarily conserved seven-pass transmembrane
RL receptor and is expressed during mouse embryonic development.*;
Mech. Dev. 78:91-95(1998).
RN [2]
RP TISSUE SPECIFICITY.
RX STRAIN-C57BL/6; TISSUE-Brain;
RX MEDLINE=97480720; PubMed=9339365;
RA Hadjantonakis A.-K., Sheward W.J., Hammar A.J., de Galan L.,
RA Hoovers J.M.N., Little P.F.R.;
RT 'Celstr', a neural-specific gene encoding an unusual seven-pass
RT transmembrane receptor, maps to mouse chromosome 15 and human
RL chromosome 22qter.*;
Genomics 45:97-104(1997).
RN [3]
RP DEVELOPMENTAL STAGE.
RX PubMed=11850187;
RA Tissier F., DeBacker O., Goffinet A.M., Lambert de Rouvroit C.A.;
RT 'Developmental expression profiles of Celstr (Flamingo) genes in the
RL mouse.*';
Mech. Dev. 112:157-160(2002).
CC -1- FUNCTION: Receptor that may have an important role in cell/cell
CC signaling during nervous system formation.
CC -1- SUBCELLULAR LOCATION: Integral membrane protein.
CC -1- DEVELOPMENTAL STAGE: First detected at E6. Predominantly expressed
CC in the developing CNS, the emerging dorsal root ganglia and
CC cranial ganglia. In the CNS, expression is uniform along the
CC rostrocaudal axis. During gastrulation, it is expressed in the
CC vicinity of the primitive streak, and becomes predominant in that
CC area at late gastrulation. At E10, detected in ventricular zones
CC (VZ), but not in marginal zones (MZ), and weakly in other
CC structures. Between E12 and E15, a high expression is present in
CC the VZ in all brain areas. No expression in differentiated
CC neuronal fields. In the newborn and postnatal stages, expression
CC remains restricted to the VZ. Also found weakly in fetal lungs,
CC kidney and epithelia.
CC -1- TISSUE SPECIFICITY: Expressed in the brain, where it is localized
CC principally in the ependymal cell layer, choroid plexus and the
CC area postrema. Also found in spinal chord and in the eye.
CC -1- SIMILARITY: BELONGS TO FAMILY 2 OF G-PROTEIN COUPLED RECEPTORS.
CC -1- SIMILARITY: CONTAINS 9 CADHERIN DOMAINS.
CC -1- SIMILARITY: CONTAINS 8 EGF-LIKE DOMAINS.
CC -1- SIMILARITY: CONTAINS 2 LAMININ EGF-LIKE DOMAINS.
CC -1- SIMILARITY: CONTAINS 1 LAMININ EGF-LIKE DOMAIN.
CC -1- SIMILARITY: CONTAINS 1 GPS DOMAIN.

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OY      5 CSONEYFDSLHACIPQJRCSS-WTPPLTQCRVC 38
Db      1199 CSESEFTSOYEGOCRCPCAHSCSCGNPADTCTSC 1233

RESULT 13
YB40_HUMAN
ID      YB40_HUMAN          STANDARD;          PRT;          708 AA.
AC      OGULT0;
DT      16-OCT-2001 (Rel. 40, Created)
DT      16-OCT-2001 (Rel. 40, Last sequence update)
DT      15-JUN-2002 (Rel. 41, Last annotation update)
DE      Hypothetical protein KIAA1140 (Fragment).
GN      KIAA1140.
OS      Homo sapiens (human).
OC      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC      Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
OX      NCBI_TaxID=9606;
RN      [1]
RP      SEQUENCE FROM N.A.
RC      TISSUE=Brain;
RA      MEDLINE=20039618; PubMed=10574461;
RA      Hirosewa M., Nagase T., Ishikawa K.-I., Kikuno R., Nomura N.,
RA      Ohara O.;
RT      "Characterization of cDNA clones selected by the Genemark analysis
RT      from size-fractionated cDNA libraries from human brain.";
RL      DNA Res. 6:329-336(1999).
CC      -1- SIMILARITY: CONTAINS 8 TPR REPEATS.
CC      -----
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CC      between the Swiss Institute of Bioinformatics and the EMBL outstation -
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CC      -----
DR      EMBL; AB032966; BA86454.1; -.
DR      InterPro; IPR001440; TPR.
DR      Pfam; PF00515; TPR; 7.
DR      SMART; SM00028; TPR; 3.
KW      Hypothetical protein; Repeat; TPR repeat.
FT      FT
FT      NON_TPR              1
FT      REPEAT              27      60      TPR 1.
FT      REPEAT              264     287      TPR 2.
FT      REPEAT              347     381      TPR 3.
FT      REPEAT              383     415      TPR 4.
FT      REPEAT              416     449      TPR 5.
FT      REPEAT              595     628      TPR 6.
FT      REPEAT              630     662      TPR 7.
FT      REPEAT              663     696      TPR 8.
FT      REPEAT
SQ      SEQUENCE      708 AA; 79140 MW; 8B93440B522CFC1C CRC64;

Query Match      23.8%; Score 57; DB 1; Length 708;
Best Local Similarity 36.8%; Pred. No. 8.7;
Matches 14; Conservative 6; Mismatches 16; Indels 2; Gaps 1.

OY      5 CSONEYFDSLHACIPQJRCSS-WTPPLTQCRVC 42
Db      277 CGKSAVAVSLLRGV--KLRPDPPTPLMAKKVCGSL 312

RESULT 14
GAS3_ARATH
ID      GAS3_ARATH          STANDARD;          PRT;          99 AA.
AC      P46687;
DT      01-NOV-1995 (Rel. 32, Created)
DT      01-NOV-1995 (Rel. 32, Last sequence update)
DT      16-OCT-2001 (Rel. 40, Last annotation update)
DE      Glbberellin-regulated protein 3 precursor.
DE      GAS3 OR ATG4G09600 OR T25P22.40.

```

OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota: Viridiplantae: Streptophyta: Embryophyta: Tracheophyta:
OC Spermatophyta: Magnoliophyta: eudicotyledons: core eudicots: Rosidae;
OC eudicots 11: Brassicales: Brassicaceae: Arabidopsis.
OX NCBI_TaxId=3702;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-CV. Columbia; TISSUE=Seed;
RC MEDLINE=95244835; PubMed=7727151;
RX Herzog M., Dorné A.-M., Grellet F.;
FT "GASA, a gibberellin-regulated gene family from Arabidopsis thaliana
RT related to the tomato GAST1 gene.";
RL Plant Mol. Biol. 27:743-752(1995).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN-CV. Columbia;
RC MEDLINE=20083448; PubMed=10617198;
RX Meyer K.F.X., Schnell C., Mamuth R., Murphy G., Volckaert G.,
RA Pohl T., Duesterhoeft A., Stiekema W., Entian K.-D., Terryn N.,
RA Harris B., Anstorge W., Brandt P., Grivell L.A., Rieger M.,
RA Weitschjager N. M., de Simone V., Obermaier B., Maché R., Mueller M.,
RA Kreis M., Delany N., Puigdomenech P., Watson M., Schmidheini T.,
RA Reichert B., Portetelle D., Perez-Alonso M., Boutry M., Bancroft I.,
RA Vos P., Hohsiehl J., Zimmermann W., Wedler H., Ridley P.,
RA Langham S.-A., McCullagh B., Blahm L., Robben J.,
RA Van der Schueren J., Grymopreisz B., Chang Y.-J., Vandenbusche F.,
RA Brecken M., Weltjens I., Voet M., Bastiaens I., Aert R., Delfor E.,
RA Melzenegger T., Botne G., Ransperger U., Hilbert H., Braun M.,
RA Holzner E., Brandt A., Peters S., van Staveren M., Dierse P.,
RA Mooliman P., Klein Linkhorst R., Rose M., Hauf J., Koeltje P.,
RA Bernsteler S., Hempel S., Feldpausch M., Lambert S., Van den Daele H.,
RA de Keyser A., Buysbaert C., Giejen J., Villarroel R., De Clercq R.,
RA Van Montagu M., Rogers J., Cronin A., Quail M., Bray-Allen S.,
RA Clark L., Doggett J., Hall S., Kay M., Leonard N., McKay K., Mayes R.,
RA Petters A., Rajandream M.A., Lyne M., Benes V., Reichmann S.,
RA Borkova D., Bloeker H., Schafte M., Grimm M., Loehnert T.-H.,
RA Dose S., de Haan M., Maarse A.C., Schaefer M., Mueller-Auer S.,
RA Gabel C., Fuchs H., Fairmann B., Granderath K., Drauner D., Herzl A.,
RA Neumann S., Agrifolou A., Vitale D., Liguori R., Piravandi E.,
RA Messner O., Quigley F., Clabaud G., Mündlein A., Felber R.,
RA Schmal S., Hiller R., Schmidt W., Lecharny A., Aubourg S.,
RA Cheifor F., Cooke R., Berger C., Monfort A., Casacuberta E.,
RA Gibbons T., Weber N., Vandenbol M., Barges M., Terol J., Torres A.,
RA Perez-Perez A., Purnelle B., Bent E., Johnson S., Tacon D., Jesse T.,
RA Heijnen L., Schwarz S., Scholler P., Haber S., Francis P., Biele C.,
RA Frishman D., Haase D., Lemcke K., Kewes H.-W., Stocker S.,
RA Zaccaria P., Devan K., Wilson R.K., de la Bastide M., Habermann K.,
RA Parnell L., Dehla N., Gnoj L., Schutz K., Huang E., Spielgel L.,
RA Sekhon M., Murray J., Sheel P., Cordes M., Abu-Threideh J.,
RA Stonelike T., Kalicki J., Graves T., Harmon G., Edwards J.,
RA Larellle P., Courtney L., Clout J., Abbott A., Scott K., Johnson D.,
RA Minx P., Bentley D., Fulton L., Miller N., Greco T., Kemp K.,
RA Kramer J., Fulton L., Mardis E., Dante M., Pepin K., Hillier L.,
RA Nelson J., Spielch J., Ryan E., Andrews S., Gelsel C., Layman D.,
RA Du H., Ali J., Bernghoff A., Jones K., Droné K., Cotton M., Joshi C.,
RA Antoniou B., Zidanic M., Strong C., Sun H., Lamer B., Yordan C.,
RA Ma P., Zhong Y., Preston R., Vil D., Shekher M., Matero A., Shah R.,
RA Shaby I.K., O'Shaughnessy A., Rodriguez M., Hoffman J., Tili S.,
RA Grant S., Shady N., Hasegawa A., Hamed A., Lohli M., Johnson A.,
RA Chen E., Marra M., Martienssen R., McCombe W.R.;
RT "Sequence and analysis of chromosome 4 of the plant Arabidopsis
thaliana".
RL Nature 402:769-777(1999).
CC -1- FUNCTION: INVOLVED IN LATE STAGES OF SEED MATURATION, OR IN EARLY
CC STEPS OF GERMINATION.
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- TISSUE SPECIFICITY: SILICOES AND DRY SEEDS.
CC -1- PTM: SIX DISULFIDE BONDS MAY BE PRESENT.
CC -1- SIMILARITY: BELONGS TO THE GAST1 FAMILY.
CC
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OY 5 CSONEVFDSLHACIP-CO---LRCSNTPPLTCORYC 38
| | : : | : : | | : | : | | : |
Db 1851 CSNHSYTTSCVPSCLPSCODPEGOCCTGAGAPSTCEBGC 1888

Search completed: November 12, 2002, 16:59:01
Job time : 5.60515 secs

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OM protein - protein search, using sw model

Run on: November 12, 2002, 16:56:16 : Search time 12.7983 Seconds
(without alignments)
676.183 Million cell updates/sec

Title: US-09-848-271-2_COPY_4_45
Perfect score: 239
Sequence: 1 MAGCQSONEYFDLSLHACIP.....LRCSSNTPPLPCQRYCNASV 42

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 671580 seqs, 206047115 residues

Total number of hits satisfying chosen parameters: 671580

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

1: sp_archaea:*
2: sp_bacteria:*
3: sp_fungi:*
4: sp_human:*
5: sp_invertebrate:*
6: sp_mammal:*
7: sp_mhc:*
8: sp_organelle:*
9: sp_phage:*
10: sp_plant:*
11: sp_protent:*
12: sp_virus:*
13: sp_vertebrate:*
14: sp_unclassified:*
15: sp_virus:*
16: sp_bacteriap:*
17: sp_archaeap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	72.5	30.3	499	11	088714
2	69.5	29.1	5374	11	099ND0
3	68	28.5	718	5	09B107
4	66	27.6	966	5	022378
5	65	27.2	2551	4	08WMO8
6	63	26.4	175	11	08R4W8
7	63	26.4	341	11	09QJ51
8	61.5	25.7	1299	5	026489
9	60.5	25.3	353	5	09VW81
10	60.5	25.3	353	5	08S258
11	60	25.1	5146	6	08SPM4
12	59.5	24.9	548	5	09GQ45
13	59.5	24.9	3034	11	035161
14	59	24.7	62	5	077419
15	59	24.7	330	5	018118
16	59	24.7	937	5	09GVR5

17	59	24.7	1717	5	026566	026566 schistosoma
18	58.5	24.5	798	5	09VTR9	09VTR9 drosophila
19	58	24.3	532	5	017496	017496 ascaris suu
20	58	24.3	1513	5	017970	017970 caenorhabdi
21	57.5	24.1	1376	5	08S252	08S252 drosophila
22	57.5	24.1	1679	5	024301	024301 drosophila
23	57	23.8	321	10	09NAM0	09NAM0 arabidopsis
24	57	23.8	387	13	09PYD4	09PYD4 xenopus lae
25	57	23.8	450	4	09B053	09B053 homo sapien
26	57	23.8	502	5	017692	017692 caenorhabdi
27	57	23.8	653	10	09S5J8	09S5J8 arabidopsis
28	57	23.8	752	4	09C091	09C091 homo sapien
29	57	23.8	838	5	027422	027422 caenorhabdi
30	57	23.8	838	5	018761	018761 caenorhabdi
31	57	23.8	955	4	096DN2	096DN2 homo sapien
32	57	23.8	1511	5	09B21	09B21 drosophila
33	56.5	23.6	146	12	09EP28	09EP28 hepatitis c
34	56.5	23.6	1792	13	057484	057484 gallus gall
35	56.5	23.6	2820	5	09VLR6	09VLR6 drosophila
36	56	23.4	260	10	08R284	08R284 oryza sativ
37	56	23.4	2972	5	090891	090891 caenorhabdi
38	55.5	23.2	146	12	09EP23	09EP23 hepatitis c
39	55.5	23.2	225	5	09VE40	09VE40 drosophila
40	55.5	23.2	675	10	094L03	094L03 oryza sativ
41	55.5	23.2	881	10	094L06	094L06 oryza sativ
42	55.5	23.2	989	10	092C00	092C00 arabidopsis
43	55.5	23.2	2843	4	09Y6R7	09Y6R7 homo sapien
44	55	23.0	160	5	09N9Q8	09N9Q8 leishmania
45	55	23.0	263	15	09WEJ8	09WEJ8 human immun

ALIGNMENTS

RESULT 1
ID 088714 PRELIMINARY: PRT: 499 AA.
AC 088714:
DT 01-NOV-1998 (TREMBLrel. 08, Created)
DT 01-NOV-1998 (TREMBLrel. 08, Last sequence update)
DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)
DE Gastric mucin-like protein (Fragment).
GN GASTRIC MUCIN-LIKE.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=STOMACH;
RA Tomasetto C., Masson R., Wendling C., Lefebvre O., Chenard M.P.,
RA Rio M.C.;
RT "Identification of interactions between trefoil peptides and members
of the mucin protein family using the yeast two-hybrid system.";
RT Submitted (SEP-1998) to the EMBL/GenBank/DBJ databases.
DR EMBL: AY010752; CA09343.1; -
DR HSSP: P5682; 1CCV.
DR InterPro: IPR002919; TIL-Cysrich.
DR InterPro: IPR001846; VWF_D.
DR Pfam: PF01826; TIL: 1.
DR Pfam: PF00094; vwd: 1.
DR SMART: SM00216; vwd: 1.
FT NON_TER 1 499
FT NON_TER 1 499
SQ SEQUENCE 499 AA: 54190 MW: 04F89EFAFF23BE61E CRC64;
Query Match 30.3%; Score 72.5; DB 11; Length 499;
Best local similarity 48.3%; Pred. No. 0.013;
Matches 14; Conservative 1; Mismatches 7; Indels 7; Gaps 1;
QY 5 CSONEYFDLSLHACIPQCRSSNTPPLT 33
DB 430 CSONEYFDLSLHACIPQCRSSNTPPLT 451

```
RESULT 2
ID 099ND0 PRELIMINARY; PRT; 5374 AA.
AC 099ND0;
DT 01-JUN-2001 (TREMblrel. 17, Created)
DT 01-JUN-2001 (TREMblrel. 17, Last sequence update)
DT 01-JUN-2002 (TREMblrel. 21, Last annotation update)
DE ZAN (Zonadhesin).
GN ZAN
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=129/SV;
RX MEDLINE=21138439; PubMed=11239002;
RA Wilson M.D., Riemer C., Martindale D.W., Schnupf P., Boright A.P.,
RA Cheung T.L., Hardy D.M., Schwartz S., Scherer S.W., Tsui L.-C.,
RA Miller W., Koop B.F.;
RT "Comparative analysis of the gene-dense ACHE/TFR2 region on human
RT chromosome 7q22 with the orthologous region on mouse chromosome 5."
RL Nucleic Acids Res. 29:1352-1365(2001).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=129/SV;
RA Cheung T.L., Wilson M.D., Koop B.F., Hardy D.M.;
RT "Genomic Basis of Inter- and Intra-species Variation in Zonadhesin
RT Domain Structure."
RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
CC - SIMILARITY: CONTAINS 3 MAM DOMAINS.
DR EMBL: AF312033; AAK28824.1; -
DR EMBL: AY046056; AAL04416.1; -
DR MGD: MG1:106656; ZAN.
DR InterPro: IPR000561; EGF-like.
DR InterPro: IPR003645; FOLN.
DR InterPro: IPR000998; MAM_domain.
DR InterPro: IPR003328; TILA_Cysrich.
DR InterPro: IPR002919; TIL_Cysrich.
DR InterPro: IPR001007; VWF_C.
DR InterPro: IPR001846; VWF_D.
DR Pfam: PF00629; MAM; 3.
DR Pfam: PF01826; TIL; 25.
DR Pfam: PF02345; TILA; 25.
DR Pfam: PF00094; vwf; 4.
DR SMART: SM00001; EGF-like; 1.
DR SMART: SM00274; FOLN; 21.
DR SMART: SM00137; MAM; 3.
DR SMART: SM00214; VWC; 25.
DR SMART: SM00216; VMD; 4.
DR PROSITE: PS00022; EGF_1; UNKNOWN_1.
DR PROSITE: PS01186; EGF_2; 18.
DR PROSITE: PS00060; MAM_2; 3.
DR EGF-like domain; Glycoprotein.
KW SEQUENCE 5374 AA; 579536 MW; 90D2B8CF5DE24EB CRC64;
SQ

Query Match 29.1%; Score 69.5; DB 11; Length 5374;
Best Local Similarity 36.8%; Pred. No. 0.37;
Matches 14; Conservative 5; Mismatches 16; Indels 3; Gaps 2;
```

```
DT 01-DEC-2001 (TREMblrel. 19, Last annotation update)
DE putative cysteine surface protein (fragment).
GN CSP.
OS Entamoeba histolytica.
OC Eukaryota; Entamoebidae; Entamoeba.
OX NCBI_TaxID=5759;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=HMI:IMS8;
RX MEDLINE=21428166; PubMed=11545438;
RA Willhoelt U., Campos-Gongora E., Touznal S., Bruchhaus I., Tannich E.;
RT "Intons of Entamoeba histolytica and Entamoeba dispar."
RL Protist 152:149-156(2001).
DR EMBL: AJ409106; CAC34072.1; -
DR InterPro: IPR002174; Furin-like.
DR SMART: SM00261; FU; 7.
DR NON TER 718
RP SEQUENCE 718 AA; 80231 MW; FFF6362M49F2827A CRC64;
SQ

Query Match 28.5%; Score 68; DB 5; Length 718;
Best Local Similarity 28.6%; Pred. No. 0.09;
Matches 12; Conservative 6; Mismatches 24; Indels 0; Gaps 0;

QY 1 MAGCSONEYFDSLHACIPCOLRCSSNTPPTCORCNASY 42
: 1:1 ||| | | | | | | | | | | | | | | | |
DB 137 LCGRCNDGSYFDSFTTRTCCKCFNCELCTSTNCFKCSNKRI 178

RESULT 4
ID 022378 PRELIMINARY; PRT; 966 AA.
AC 022378;
DT 01-NOV-1996 (TREMblrel. 01, Created)
DT 01-OCT-2001 (TREMblrel. 18, Last sequence update)
DT 01-JUN-2002 (TREMblrel. 21, Last annotation update)
DE Hypothetical 102.5 kDa protein.
GN T10E10.4.
OS Caenorhabditis elegans.
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
OC Rhabditidae; Peloderinae; Caenorhabditis.
OX NCBI_TaxID=6239;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=BRISTOL N2;
RX MEDLINE=99069613; PubMed=9851916;
RA None;
RT "Genome sequence of the nematode C. elegans: a platform for
RT investigating biology. The C. elegans Sequencing Consortium."
RL Science 282:2012-2018(1998).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=BRISTOL N2;
RA Gettel C.;
RT "The sequence of C. elegans cosmid T10E10."
RL Submitted (NOV-1995) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN=BRISTOL N2;
RA Waterston R.;
RT "Direct Submission."
RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL: U99644; AAB0360.2; -
DR HSSP: P10969; IWTG.
DR InterPro: IPR002557; Chitin_bind_Pera.
DR InterPro: IPR000794; Ketoacyl-synt.
DR InterPro: IPR003571; Snake_toxin.
DR InterPro: IPR002899; WRI/EB.
DR Pfam: PF01607; CBM_14; 2.
DR SMART: SM00289; WRI; 12.
DR PROSITE: PS00606; B_KETOACYL_SYNTHASE; UNKNOWN_1.
DR PROSITE: PS00272; SNAKE_TOXIN; UNKNOWN_1.
KW Hypothetical protein.
SQ SEQUENCE 966 AA; 102460 MW; B565A3CDD5216D9 CRC64;
```

Query Match 27.6%; Score 66; DB 5; Length 966;
 Best Local Similarity 39.4%; Pred. No. 0.24;
 Matches 13; Conservative 7; Mismatches 11; Indels 2; Gaps 1;

OY 4 QCSQNEFYDSLHACIPCOLR-CSSNTPPLTC 34
 DB 215 QCSQSTVFNSDLNVCVPIALIQNSCDSSTQOPVC 247

RESULT 5

O8MW08 PRELIMINARY; PRT; 2551 AA.

AC O8MW08;
 DT 01-MAR-2002 (TREMBLrel. 20, Last sequence update)
 DT 01-MAR-2002 (TREMBLrel. 21, Last sequence update)
 DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)
 DE Stabilin-2.
 GN STAB2.
 OS Homo sapiens (human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Polit O., Gratchev A., McCourt P.A.G., Schledzinski K., Guillot P.,
 RA Johansson S., Birk R., Hakly N., Franke P., Kodelya V., Kammicht C.,
 RA Orfanos C.E., Johansson S., Goerd S.;
 RT "Stabilin-1 and stabilin-2 constitute a novel family of fasciclin-
 domain-containing adhesion molecules associated with endothelial-
 RT macrophage differentiation and angiogenic processes";
 RL Submitted (JUL-2000) to the EMBL/Genbank/DBJ databases.
 DR EMBL: AJ295695; CACB105.1;
 DR InterPro: IPR000782; B19H3_Fasciclin.
 DR InterPro: IPR000561; EGF-like.
 DR InterPro: IPR002049; Laminin-EGF.
 DR InterPro: IPR000538; Link.
 DR Pfam: PF00008; EGF; 20.
 DR Pfam: PF02469; Fasciclin; 5.
 DR Pfam: PF00193; Xlink; 1.
 DR ProDom: PD000918; Link; 1.
 DR SMART: SM00181; EGF; 24.
 DR SMART: SM00445; Link; 1.
 DR PROSITE: PS00022; EGF_1; UNKNOWN_7.
 DR PROSITE: PS01186; EGF_2; UNKNOWN_16.
 DR PROSITE: PS01248; LAMININ_TYPE_EGF; UNKNOWN_2.
 SO SEQUENCE 2551 AA; 276992 MW; 60A44651CC2BE69 CRC64;

Query Match 27.2%; Score 65; DB 4; Length 2551;
 Best Local Similarity 30.0%; Pred. No. 0.86;
 Matches 13; Conservative 4; Mismatches 9; Indels 22; Gaps 2;

OY 15 LHACIPCOLR-CSSNTPPLTC-CORVCNASV 42
 DB 674 LGTCVCSLVYWRCPANSEPTALFTRHCYSGRFGSLKSGCARFCNMTFV 723

RESULT 6

O8R4W8 PRELIMINARY; PRT; 175 AA.

AC O8R4W8;
 DT 01-JUN-2002 (TREMBLrel. 21, Created)
 DT 01-JUN-2002 (TREMBLrel. 21, Last sequence update)
 DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)
 DE TRAF3 binding protein.
 OS Mus musculus (mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Mizuno K., Irie S., Sato T.-A.;
 RT "Identification of novel TRAF3 binding protein, T3BP, which increases

RT cellular F-actin content.";
 RL Submitted (FEB-2001) to the EMBL/Genbank/DBJ databases.
 DR EMBL: AF350257; AAL8314.1;
 SO SEQUENCE 175 AA; 18846 MW; B64EFF4B52EE93B1 CRC64;

Query Match 26.4%; Score 63; DB 11; Length 175;
 Best Local Similarity 50.0%; Pred. No. 0.13;
 Matches 10; Conservative 4; Mismatches 6; Indels 0; Gaps 0;

OY 4 QCSQNEFYDSLHACIPCOLR 23
 DB 21 QCSQNEFYDSLHACIPCOLR 40

RESULT 7

ID Q9D351 PRELIMINARY; PRT; 341 AA.

AC Q9D351;
 DT 01-JUN-2001 (TREMBLrel. 17, Created)
 DT 01-JUN-2001 (TREMBLrel. 17, Last sequence update)
 DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)
 DE 7420700M05RIK protein.
 GN 7420700M05RIK.
 OS Mus musculus (mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STEADY-STATE IN VITRO FERTILIZED EGGS;
 RX MEDLINE=21085660; PubMed=11217851;
 RA Kawai J., Shingawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
 RA Arkava T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
 RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamahata I.,
 RA Saito T., Okazaki Y., Gojibori T., Bono H., Kasukawa T., Saito R.,
 RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Kasavan T.,
 RA Fiedlermann W., Gaasterland T., Glass C., King B., Kochava H.,
 RA Kuhl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
 RA Schirral L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,
 RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barh G.,
 RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
 RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gaitanaris M.,
 RA Gustincich S., Hill D., Hornann M., Hume D.A., Kamiya M., Lee N.H.,
 RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,
 RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
 RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
 RA Suzuki H., Toyooka K., Wang K.H., Weitz C., Whitaker C., Wilming L.,
 RA Wyshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohsaki S.,
 RA Hayashizaki Y.,
 RT "Functional annotation of a full-length mouse cDNA collection.";
 RL Nature 409:685-690(2001).
 DR EMBL: AK018361; BAB31177.1;
 DR HSSP: P08047; ISP1.
 DR MGD: MGI:1923003; 7420700M05RIK.
 DR InterPro: IPR000823; Znf_C2H2.
 DR Pfam: PF00096; Zf-C2H2; 3.
 DR ProDom: PD000003; Znf_C2H2; 1.
 DR SMART: SM00355; Znf_C2H2; 3.
 DR PROSITE: PS00028; ZINC_FINGER_C2H2_1; 2.
 DR PROSITE: PS0157; ZINC_FINGER_C2H2_2; 3.
 SO DNA-binding; Metal-binding; Zinc-finger.
 KW SEQUENCE 341 AA; 38094 MW; A332DB7FE231AFPC CRC64;

Query Match 26.4%; Score 63; DB 11; Length 341;
 Best Local Similarity 28.2%; Pred. No. 0.25;
 Matches 11; Conservative 9; Mismatches 19; Indels 0; Gaps 0;

OY 4 QCSQNEFYDSLHACIPCOLR-CSSNTPPLTC-CORVCNASV 42
 DB 59 RCNEREMESQILRSLPBGVRCPSOLAPIFQVNCORSI 97

RESULT 8

Matches 14; Conservative 5; Mismatches 15; Indels 11; Gaps 2;

OY 4 OCSQNEFYDSLHACIPCOL---RCSSNTP-----PLTCORY 37
 DB 118 KCSVNYFDPARRACLPVIAISAHQCSCVLPDNIATLANSDECETY 162

RESULT 11

O8SPM4 ID O8SPM4 PRELIMINARY; PRT; 5146 AA.

AC Q8SPM4; 01-JUN-2002 (TREMBLrel. 21, Created)

DT 01-JUN-2002 (TREMBLrel. 21, Last sequence update)

DE 01-JUN-2002 (TREMBLrel. 21, Last annotation update)

GN SCO-SPONDIN.

OS Bos taurus (Bovine).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;

OC Bovidae; Bovinae; Bos.

OX NCBI_TaxID=9913;

RP [1]

RC TISSUE-SUBCOMMISSURAL ORGAN;

RA Submitted (OCT-2001) to the EMBL/GenBank/DBJ databases.

RN [2]

RP SEQUENCE FROM N.A.

RC TISSUE-SUBCOMMISSURAL ORGAN;

RA MEDLINE-20465125; PubMed-11008217;

RT Gobion S.;

RT *Subcommissural organ/Reissner's fiber complex: characterization of

RT SCO-SPONDIN, a glycoprotein with potent activity on neurite

RT outgrowth.;

RL Gila 32:177-191(2000).

RL EMBL: AJ416457; CAC94914.1;

SO SEQUENCE 5146 AA; 543576 MW; 724C5FB8727B13DA CRC64;

Query Match 25.1%; Score 60; DB 6; Length 5146;

Best Local Similarity 42.9%; Pred. No. 9 6;

Matches 9; Conservative 3; Mismatches 9; Indels 0; Gaps 0;

OY 14 LHACIPCOLRCSSNTPPLTC 34

DB 1814 VFHACVPCPLTCDDISQATC 1834

RESULT 12

O9GQ45 ID O9GQ45 PRELIMINARY; PRT; 548 AA.

AC Q9GQ45; 01-MAR-2001 (TREMBLrel. 16, Created)

DT 01-MAR-2001 (TREMBLrel. 16, Last sequence update)

DE 01-JUN-2002 (TREMBLrel. 21, Last annotation update)

DE Variant-specific surface protein M2-1 (Fragment).

GN M2-1.

OS Giardia lamblia (Giardia intestinalis).

OC Eukaryota; Diplomonadida; Hexamitidae; Giardinales; Giardia.

OC NCBI_TaxID=5741;

OX [1]

RP SEQUENCE FROM N.A.

RC STRAIN-AD-1;

RA Mansouri M., Ey P.L.;

RT *A segment of a vsp72-like gene homolog from a type A-1 (group 1)

RT Giardia intestinalis isolate.;

RL Submitted (AUG-2000) to the EMBL/GenBank/DBJ databases.

DR EMBL: AF298862; AAC37862.1;

DR HSSP: P00136; 2c73.

DR InterPro: IPR000564; 2Fe2S-ferredoxin.

DR InterPro: IPR000345; Cytc_heme_bind.

DR InterPro: IPR000561; EGF-like.

DR InterPro: IPR002174; Furin-like.

DR InterPro: IPR002350; Kazal.

DR SMART: SM00181; EGF_2.

DR SMART: SM00001; EGF_Like; 1.

DR SMART: SM00261; FU; 5.

DR PROSITE: PS00197; 2FE2S-FERREDOXIN; UNKNOWN_1.

DR PROSITE: PS00190; CYTOCHROME_C; UNKNOWN_1.

DR PROSITE: PS00282; KAZAL; UNKNOWN_1.

FT NON_TER 1 1

FT NON_TER 548 548

FT SEQUENCE 548 AA; 56557 MW; 578FE4EDA0A2CF0E CRC64;

Query Match 24.9%; Score 59.5; DB 5; Length 548;

Best Local Similarity 36.6%; Pred. No. 1 3;

Matches 15; Conservative 4; Mismatches 15; Indels 7; Gaps 2;

RESULT 13

O35161 ID O35161 PRELIMINARY; PRT; 3034 AA.

AC O35161; 01-JAN-1998 (TREMBLrel. 05, Created)

DT 01-MAY-1999 (TREMBLrel. 10, Last sequence update)

DE 01-JUN-2002 (TREMBLrel. 21, Last annotation update)

DE Seven-pass transmembrane receptor precursor.

GN CELSR1.

OS Mus musculus (Mouse).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

OX NCBI_TaxID=10090;

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN-C57/BL6; TISSUE-BRAIN;

RA MEDLINE-97480720; PubMed-9339365;

RA Hadjantonakis A.K., Sheward W.J., Harmar A.J., de Galan L.,

RA Hoovers J.M., Little P.F.;

RT *Celsr1, a neural-specific gene encoding an unusual seven-pass

RT transmembrane receptor, maps to mouse chromosome 15 and human

RT chromosome 45:97-104(1997).

RL Genomics 45:97-104(1997).

RL EMBL: AF031572; AAC68836.1;

DR HSSP: P00749; IURK.

DR MGI: MGI1100883; Celsr1.

DR InterPro: IPR000152; Asx_hydroxyl.

DR InterPro: IPR002126; Cadherin.

DR InterPro: IPR000561; EGF-Like.

DR InterPro: IPR000832; GPCR_secretin.

DR InterPro: IPR001879; hormu_receptor.

DR InterPro: IPR002049; laminin_EGF.

DR InterPro: IPR001791; laminin_G.

DR InterPro: IPR000203; PKD_cys_rich.

DR Pfam: PF000028; cadherin. 9.

DR Pfam: PF00008; EGF_6.

DR Pfam: PF01825; GPS; 1.

DR Pfam: PF02793; HRM; 1.

DR Pfam: PF00053; laminin_EGF_1.

DR Pfam: PF00054; laminin_G_1.

DR PRINTS: PR00205; CADHERIN.

DR PRINTS: PR00011; EGF_LAMININ.

DR PRINTS: PR00249; GPCRESECRETIN.

DR SMART: SM00112; CA; 9.

DR SMART: SM00180; EGF_Lam; 1.

DR SMART: SM00001; EGF_Like; 6.

DR SMART: SM00303; GPS; 1.

DR SMART: SM00008; Horm; 1.

DR SMART: SM00282; Lamg; 2.

DR PROSITE: PS00010; ASX_HYDROXYL; UNKNOWN_2.

DR PROSITE: PS00232; CADHERIN_1; 6.

DR PROSITE: PS0268; CADHERIN_2; 9.

[illegible]